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(71) Applicant: **CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).**(72) Inventors: **XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).**(74) Agents: **MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).**(81) Designated States: **AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).****Published***Without international search report and to be republished upon receipt of that report.*(54) Title: **COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE**

## (57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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## COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

### TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos. 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from



suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (i.e., the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (i.e., at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. See, *e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.



Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereof. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (i.e., a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1  $\mu$ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### EXAMPLE 1

##### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size



being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of H<sub>2</sub>O, heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l H<sub>2</sub>O. Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l H<sub>2</sub>O, mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO: 73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively; and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA<sup>+</sup> RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively).

Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## EXAMPLE 2

## DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first-strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTON

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant



homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain); and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### EXAMPLE 4

##### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun  
Dillon, Devin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SEED and BERRY LLP
  - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
  - (C) CITY: Seattle
  - (D) STATE: WA
  - (E) COUNTRY: USA
  - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 23-FEB-1998
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Maki, David J.
  - (B) REGISTRATION NUMBER: 31,392
  - (C) REFERENCE/DOCKET NUMBER: 210121.428C3
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 622-4900
  - (B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCTGTGT	GAAATTGTTA	TCCGCTCACA	480
ATTCCACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAG	CCTGGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAAGTGTCTG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTTGGG	TTTTGGGGGGC	660
TCTTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCNTT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATENGNG	GATACCCNGG	AAAAAANTTT	780
AACAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATACGACTT	ACAGGACAGC	AGATGGGGAA	60
TTTCATGGCTG	TTGGAGCAAT	AGAACCCAG	TTCTACGAGC	TGCTGATCAA	AGGAATTGGA	120
CTAAAGTCTG	ATGAACCTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTTGCAG	ATGTATTTGC	AAAGAAGACG	AAGGCAGAGT	GGTGTCAAAT	CTTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCAATC	TGATCACAAC	300
AAGGAACGGG	GCTCGTTTAT	CACCACTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCAGC	CATCCCTTCT	TTCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCCTGT	GTGAAATGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTTAAG	CCTGGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTGCGCTCA	CTGCCCCTT	TCCAGTCGGG	AAAAGTGTCTG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTCNTT	TTGGGCTCTC	TCCGCTTTCC	720
TCGCTCATTG	ATCCTNGCNC	CCGGTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCCNGA			816

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG	AAGGGATGGC	TGGGGTGT	TTT AACAGCAGAG	GTGCAGGGCG	GGGGCTCACC	60
TCCTGCTCCT	CACGTGTGAT	AAACGAGCCC	CGTTCCTTGT	TGTGATCATG	ATGAACAACC	120

TCCTCAAAG	TCAGAACGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTTGC	AAATACATCT	GCAAACCTCT	TCTTCATTTT	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCCTTT	GATCAGCAGC	300
TCGTAGAACT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTC	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTCGCC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCTGT	TTACAACGTC	480
GTGACTGGGA	AAACCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTTCG	540
CCAGCTGGGC	GTAATANCGA	AAAGGCCCGC	ACCGATCGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNAA	ATGGGACCCC	CCTGTTACCG	CGCATTTAAC	CCCCGCNGGG	TTTNGTTGTT	660
ACCCCCACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCGCTCCC	TTTCNCCTTT	720
CTTCCCCTTC	TTTCNCNCCN	CTTTCCCCCG	GGGTTTCCCC	CNTCAAACCC	CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT	CCTACTGACC	TGTGCTTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTT	GTCCTCTCCT	120
TCGGAAACAT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCTT	360
GNGGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTTGTT	CCCTTTAGTG	AGGGTTAATT	480
GCGCGCTTGG	CNTAATCATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCCGTTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGCA	TNATGAATCN	GCCAACCCCC	GGGGAAAGC	GTTTGCGTTT	TGGGCGCTCT	720
TCCGCTTCCT	CNCTCANTTA	NTCCCTNCNC	TCCGTCAATC	CGGCTGCNGC	AAACCGGTTT	780
ACCNCTTCCA	AAGGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTTAATT	GCATCCAAAG	TACTAACAAA	AACCTTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAAATTGGT	TTTCATAAGA	TAATTTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTTGGCA TAAACAATAA TAAAACAATC ACAATTTAAT AAATAACAAA TACAACATTG	300
TAGGCCATAA TCATATACAG TATAAGGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG	360
AATAGAATAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTTGATTAC TCAGCCCTGA	420
CATTCAGTTT TCAAAGTAGG AGACAGGTTT TACAGTATCA TTTTACAGTT TCCAACACAT	480
TGAAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA	540
TCACCAACCC CTCAGTTATA AAAAATTTTC AAGTTATATT AGTCATATAA CTTGGTGTGC	600
TTATTTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT	660
GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTTGA ACTGGAACAT	720
TGNATNACAG TGTTCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA	780
TGTTATTTTG TTAAAAATTA AATTTTAACC TGGTGAAAA ATAATTTGAA ATNA	834

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACCACATCT ACAAATGCC AGTATCAGGC GCGGCTTCG AAGCCAAAGT GATGTTTGGA	120
TGTAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT	180
GACGTGAAGT CCGTGGAAGC CTGTGGCTAC AAAAAATGTT GAGCCGTAGA TGCCGTCGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGTAGG AGGGTAAAT AGAGACCCAG	300
TAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTTCTA TTAGACTATG	360
GTGAGCTCAG GTGATTGATA CTCCTGATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC	420
TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TGGGGGCCAG TGCCCTCCTA GTTGGGGGGT	480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAAATCCT GCGAAGAAAA AAACCTCTGA	540
GGTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTTGG ACAGGTGGTG TGTGGTGGCC	600
TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTGGG	660
TTANTANGGC CTANTATGAA GAACCTTTGG ANTGGAATTA AATCAATNGC TTGGCCGGAA	720
GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGTCTGGG CTNGGTTTTA CCCNACCCAT	780
GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA	818

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA	60
CGGGCCCTAT TTCAAAGATT TTTAGGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT	120
GGTTTGCTCC ACAGATTTC A GAGCATTGAC CGTAGTATAC CCCCCTCGT GTAGCGGTGA	180
AAGTGGTTTG GTTTAGACGT CCGGGAATTG CATCTGTTTT TAAGCCTAAT GTGGGGACAG	240
CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGGCT TCAATCGGGA	300

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GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG 360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC 420
ATTGGTGGCC AATTGATTTG ATGGTAAGGG GAGGGATCGT TGAACCTCGTC TGTATGTAA 480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT 540
TCAAACNGTC TCTANTTCCT GAAACGTCG AAATGTTAAT AANAATTAAN TTTNGTTATT 600
GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNTAANGG 660
CNTTATCNTN AAAGGTNATA ACCNCTCCTA TNATCCCACC CAATNGNATT CCCCACNCNN 720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTGTTC 780
CTTNANTGAN GGTTATTCNC CCCTNGCNTT ATCANCC 817

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG 60
CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT 120
CTGAAGCGCA CGTCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG 180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCCTGGGG 240
TGGGTGGCCG ANGCTGANC CGCTCTGCC TGTGCCCCC ANGTTGGGCCG CCACCCCTG 300
ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCCACANGG 360
GGATTTTGCT CCTANANTAA GGCTCATCTG GGCCTCGGCC CCCCACCTG GTTGGCCTTG 420
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCNG GACCACCTTT NGGGAGTGTT 480
CTCCTTACAA CCACANNATG CCCGGCTCCT CCGGAAACC ANTCCCANCC TGNGAAGGAT 540
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGAACC CNCCTTNTGT 600
TCCTTTTCNT TNAGGGTTAA TNNGCCTTG GCCTTNCAN NGTCTTNCNC NTTTTCCNNT 660
GTTNAAATTG TTANGCNCCC NCCNNTCCN CNNCNNCNA CCGACCCNN ANNTTNNANN 720
NCTGGGGGT NCCNNGAT TGACCCNCC NCCCTNTANT TGCNTTNGGG NNCNNTGCCC 780
CTTCCCTCT NGGGANNCG 799

```

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTTG 60
TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT 120
CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCACAT GATCCTTACT CTATGAGCAA 180
AATCCCCTGT GGGGCTTCT CTTGAAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG 240
CAGGTCATGG GGTGTNGNC CAACTGGGGG CCNCAACGCA AAANGGCNCA GGGCTCNGN 300
CACCCATCCC ANGACGCGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGCGCTG 360

```



TTCNTACCCG CGNATNTGTC CCANCTGTTT CNGTGCCNAC TCCANCTTCT NGGACGTGCG 420  
 CTACATACGC CCGGANTGNC NCTCCCGCTT TGTCCCTATC CACGTNGCAN CAACAAATTT 480  
 CNCCNTANTG CACCNATTC CACNTTTTNC AGNTTTCNC NNCNGGCTTC CTTNTAAAAG 540  
 GGTGAGNCCC CGGAAAATNC CCCAAAGGGG GGGGGCENG TAECCTACTN CCCCCTNATA 600  
 GCTGAANTCC CCATNACCNN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT 660  
 GGGAAANACC CTCGNCCNTN CCCCNTTAA TCCNCCTTG CNANGNNCNT CCCCNTTCC 720  
 NCCCNNTNG GCNTNTNANN CNAAAAAGGC CCNNNANCA TCTCCTNNCN CCTCANCTCG 780  
 CCANCCCTCG AAATCGGCCN C 801

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTAINT GGCCAGTGTG GCAGCTTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC 60  
 ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCTCACCGG GTTCACCTTC TCAGCCCTGC 120  
 AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGA GAAGCAGGTG TTCTGCCCCA 180  
 AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCTGC 240  
 CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGCTGGA GGCAGTGGCC 300  
 TGCTCCCACC TCCACCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG 360  
 TGGTGGGTGA GCCACCGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTEG 420  
 CCATCCTGGA TAGTGCTTCC TGCTGTCCCA NGTGGCCCCA TCCCTGTTTA TGGGCTCCAT 480  
 TGTCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCCGACGGCC TGGGTCTGGT 540  
 CCCATTACT TTGCTACACA GGTANTATTT GACAAGAAGC ANTTGGCCAA ATACTCAGCG 600  
 TTAATAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT EACTGGGTCC AACTCCCCGC 660  
 TCCTGTTAAC CCCATGGGGC TGCCGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT 720  
 GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG 780  
 GNGTTCCTC 789

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC 60  
 TTTGTAAAT AAATAAGTTA AATATTTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG 120  
 ACCAACAGGC CACATCCTGA TAAAAGGTAA GAGGGGGGTG GATCAGCAA AAGACAGTGC 180  
 TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTCA GGACTCTTCC CCTACAAATA 240  
 ACTTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAACTCC CATGCAAGAG 300  
 CTACATTAAG CGAAGCTGCA GGTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT 360  
 TATTCAGCTC CAAAAACCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTAAACC 420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGGAA	AAAAGAAAAG	GACGCCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTTA	CTTTGGCACA	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTTAACAGGA	ANCNGGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCCAC	CCCNAAATNTT	GCTGGGAAAT	TTTTCTCCCC	CTAAATNTTT	TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GGAAGTGCTC	AGCCATTGTG	GTGTACACCA	AGGCGACCAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGATCG	TCNCGAGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTCA	AAAAGGATGC	CCCATCNATT	GACCCCCCAA	ATGCCCCACTG	600
CCAACAGGGG	CTGCCCCACN	CNCNNAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCCTGCN	TNGTGGCTCC	TGTTCAAGNC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANNC	G			751

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTTCAGA	ACTCANTGCC	AAGANCCCTG	AACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCAATTT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GTCCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCTTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACCTA	TACGGATTTT	600

3AAGANTCAC CTACTTCAAA GAAAANAGTG CCTTTECCCC ATTTCTGTTG CAATTGACAA 660  
 ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAACCC AANGGGTCC CCAACCANAA 720  
 ATTNAAGGG 729

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCTT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG 60  
 TGTTTCGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGCAGAG TCCTGTGTCT 120  
 GGCAGGTCCA CGCAGTCCCC TTTGTCACTG GGGAAATGGA TGCCTGGAG CTCGTCAAAG 180  
 CCACTCGTGT ATTTTTCACA GGCAGCCTCG TCCGACGCGT CGGGGCAGTT GGGGGTGTCT 240  
 TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACTG GGTGGGCTGA 300  
 CANGTGCCAG AGCACACTGG ATGGCGCCTT TCCATGNNAN GGGCCCTGNG GGAAAGTCCC 360  
 TGANCCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACA CCCCAGACAG CTAGAATGGA 420  
 ATCTTCTTCC CGAAAGGTAG TTNTTCTTGT TGCCCAANCC ANCCCNNTAA ACAAACTCTT 480  
 GCANATCTGC TCCGNGGGGG TCNTANTACC ANCGTGGGAA AAGAACCCCA GGCNGCGAAC 540  
 CAANCTTGTT TGGATNCGAA GCNATAATCT NCTNTTCTGC TTGGTGGACA GCACCANTNA 600  
 CTGTNNANCT TTAGNCCNTG GTCTCCTGTT GTTGNNCTTG AACCTAATCN CCNNTCAACT 660  
 GGGACAAGGT AANTNGCCNT CCTTTNAAIT CCNANCTN CCCCCTGGTT TGGGGTTTTN 720  
 CNCNCTCCTA CCCCAGAAAN NCGTGTCTCC CCCCCTA GGGGCCNAAA CCNNTTNTTC 780  
 CACAACCCTN CCCCACCCAC GGGTTCNGNT GGTTNG 816

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG 60  
 ATGTGGAAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG GTAGAGAGGA 120  
 AAGACCCAAA CCAGGTGGAA CTGTGGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA 180  
 CAGTGAAGTAG CTCAGACCAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA 240  
 CCAAGCAGAC AGAAGACTAC TGCCTCGCAT CCAACAANGT GGGTCGCTGC CGGGGCTCTT 300  
 TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAA GAGTTTCGTT TATGAGGCT 360  
 GCCTGGGCAA CAAGAACAAC TACCTTCGGG AAGAAGAGTG CATTCTANCC TGTGNGGCTG 420  
 TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCTT 480  
 CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCACCCAG TTCCGCTGCA 540  
 NCAATGGCTG CTGCATCNAC ANTTTCCTNG AATTGTGACA ACACCCCCCA NTGCCCCAA 600  
 CCCTCCCAAC AAAGCTTCCC TGTNAAAAA TACNCCANTT GGCTTTTNAC AAACNCCCGG 660  
 CNCCTCCNTT TTCCCNNTN AACAAAGGGC NCTNGCNTTT GAACTGCCCN AACCNGGAA 720

TCTNCCNNGG AAAAAANTNCC CCCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC 780  
 CCC 783

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTCGGAT GTCATACAAA 60  
 AGCTGATTGA AGCAACCCTC TACTTTTGG TCGTGAGCCT TTTGCTTGGT GCAGGTTTCA 120  
 TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCACT GTTCTCTTTG 180  
 AAGTAGGGTG AGTCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC 240  
 ATGGTGGTGT TCCACACTTG AGTGAACTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA 300  
 GGCACTACCA GCAACGTCAG GAAGTGCTCA GCCATTGTGG TGTACACCAA GGCGACCACA 360  
 GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA 420  
 CACTTGCTCT CCGTCTTAGC ACCATAGCAG CCCANGAAC CAAGAGCAAA GACCACAACG 480  
 CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAACTG CATGGCCACT GGACGACAGT 540  
 TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATCGATTG AACACCCANA TGCCCACTGC 600  
 CNACAGGGCT GCNCCNCCN GAAAGAATGA GCCATTGAAG AAGGATCNTC NTGGTCTTAA 660  
 TGAAGTGAAA CCNTGCCATGG TGGCCCTGT TCAGGGCTCT TGGCAGTGAA TTCTGANAAA 720  
 AAGGAACNGC NTNAGCCCCC CCAAANGANA AAACACCCCC GGGTGTGGCC CTGAATTGGC 780  
 GGCCAAGGAN CCCTGCCCCN G 801

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA GGCCTCCCTC TGCCTGCCCA CTCAGTGGCA ACACCCGGGA GCTGTTTTGT 60  
 CCTTTGTGGA GCCTCAGCAG TTCCCTCTTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG 120  
 AGCCACCATG CAGTGCTTCA GCTTCATTAA GACCATGATG ATCCTCTTCA ATTTGCTCAT 180  
 CTTTCTGTGT GGTGCAGCCC TGTGGCAGT GGGCATCTGG GTGTCAATCG ATGGGGCATC 240  
 CTTTCTGAAG ATCTTGGGG CACTGTCGTC CAGTGCCATG CAGTTTGTC ACGTGGGCTA 300  
 CTTCTCATC GCAGCCGGCG TTGTGGTCTT TGCTCTTGGT TTCCTGGGCT GCTATGGTGC 360  
 TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT 420  
 TGCTGAAGTT GCAGCTGCTG TGGTCGCCTT GGTGTACACC ACAATGGCTG AACCATTCCT 480  
 GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACCT 540  
 AANTNTGGAA CACCNCATG AAAAGGGCTC CAATTTCTGN TGGCTTCCCC AACTATACCG 600  
 GAATTTTGAA AGANTCNCCC TACTTCCAAA AAAAAANANT TGCCTTTNCC CCCNTTCTGT 660  
 TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNCAAA 720  
 CAAAAAANT NNAAGGGTTN 740

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATAACACA GCCTCAATCA 60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG 120
GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTGGAAGC TTATTCTTCT 180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTTCAGCTAA GTAGTCAGCG TATGTCCCAT 240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA 300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT 360
GGATGAGTGT GGCCAGCGCT GCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT 420
GGTTCTGCCC TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG 480
GCTCAGGATG TCCAGAGACG TGGFTCCGCC CCCTCNCCTA ATGACACCGN CCANNCAACC 540
GTCGGCTCCC GCGGANTGNG TTCGTCTGTC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC 600
AANCTTCGTC NGGCCCATGG AATTCAACCNC ACCGGAACNT GTANGATCCA CTNNTTCTAT 660
AACCGGNCGC CACCGCANNNT GGAACCTCCAC TCTTNTNCC TTTACTTGAG GGTAAAGGTC 720
ACCTTNNCG TTACCTTGGT CCAAACNTN CCNTGTGTCG ANATNGTNAA TCNGGNCNCA 780
TNCCANCCNC ATANGAAGCC NG

```

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG 60
GAGCCCACCG TCACGNGGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT 120
CNTGACCCCA ACTCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTACGTGG 180
CAGGAACCAA GANCAAANNC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC 240
GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CTTGTCTACT TGTTTGAGA ACNGCANNNGA 300
CATGCCCAGN GTTANATAAC NGGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGCGCAN 360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCCT 420
CCACTAAGCT CAGAACAAA AACTTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA 480
AAGTGATCCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG 540
GAAGACCTAT CAATTNAAGC TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC 600
CNNCNTTCCA AGGGGGGGNC GGCCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN 660
CCCCNNGGCC CGGECTTTTA CNANCNTCNN NNACNGGGNA AAACCNNNGC TTTNCCCAAC 720
NNAATCCNCC T

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

TTTTTTTTTT TTTTTTTTTT TAAAAAGCCC CTCCATTNAA TGNAAACTTC CGAAATTGTC      60
CAACCCCTTC NTCCAAATNN CCNTTTCGGG GNGGGGGTTC CAAACCCAAN TTANNTTGG      120
ANNTTAAATTT AAAATNTTNTT TGGNGGNNNA ANCCNAATGT NANGAAAGTT NAACCCANTA      180
TNANCTTNAA TNCCTGGAAA CCNGTNGNTT CCAAAAATNT TTAACCTTA ANTCCCTCCG      240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTTGTTT GAAGGNTNAA TNAAAANCCC      300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTTCC NTTAAANAA      360
GGNNANCCCC GGTANTNAA TCCCCCNC CCAATTATA CCGANTTTT TTNGAATTGG      420
GANCCNCGG GAATTAACGG GGNNNTCCC TTTTGGGGGG CNGGNNCCCC CCCNTCGGG      480
GGTNGGGNC AGGNCNNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC      540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCCC CANGGCCCT CTGCGNAGT TGGGGTTTGG      600
GGGGCCTGGG ATTTNTTTC CCCTNTTNC TCCCCCCCCC CCNGGGANAG AGGTTNGNGT      660
TTTGNTCNCN GGGCCCNCCN AAGANCTTN CCGANTTNAN TTAAATCCNT GCCTNGGCGA      720
AGTCNTTGN AGGGNTAAAN GGCCCCCTNN CGGG      754

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

ATCANCCCAT GACCCCNAAAC NNGGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA      60
NNGTNAGNNC ACTNCNNTTN NATCNCNCCC CNCCNACTAC GCCNCNANC CNACGCNCTA      120
NNCANATNCC ACTGANNGCG CGANGTNGAN NGAGAAANCT NATACCANAG NCACCANACN      180
CCAGCTGTCC NANAANGCCT NNNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN      240
NNCNCANAT GATTTTCCCTN ANCCGATTAC CCNTNCCCC TANCCCCCTCC CCCCCAACNA      300
CGAAGGCNCT GGNCCNAAGG NNGCGNCNC CCGCTAGNTC CCCNNCAAGT CNCNCNCCTA      360
AACTCANCCN NATACNCGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC      420
AAAAANATCN GATACAAAT AATNCAAGCC TGNATTATNAC ACTNTGACTG GGTCTCTATT      480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATTT CCNAANGGCT      540
CTTTCNGACA GCATNTTTTG GTTCCNNTT GGGTCTTAN NGAATGCCC TTCNTNGAAC      600
GGGCTCNTCT TTTCTTCGG TTANCCTGGN TTCNNCCGGC CAGTTATTAT TTCCNNTTTT      660
AAATTCNTNC CTTTTANTTT TGGCNTTCNA AACCCCGGC CTTGAAAACG GCCCCCTGGT      720
AAAAGGTTGT TTTGANAAAA TTTTGTTTTT GTTCC      755

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

TTTTTTTTTT TTTTANGTG TNGTCGTGCA GGTAGAGGCT TACTACAANT GTGAANACGT      60
ACGCTNNGAN TAANGCGACC CGANTTCTAG GANNCNCCCT AAAATCANAC TGTGAAGATN      120
ATCCTGNNA CGGAANGGTC ACCGGNNGAT NNTGCTAGGG TGNCCNCTCC CANNNCNTTN      180
CATAACTCNG NGGCCCTGCC CACCACCTTC GGCGGCCCG NGNCCGGGCC CGGGTCATTN      240
GNNTTAACCN CACTNNGCNA NCGGTTTCCN NCCCCNNGG ACCGNGGCGA TCCGGGGTNC      300
TCTGTCTTCC CCTGNAGCN ANAAANTGGG CCNCGNCCC CTTTACCCCT NNACAGCCA      360
CNGCCNTCTA NCCNCGCCC CCCCTCCANT NNGGGGACT GCCNANNGCT CCGTTNCTNG      420
NNACCCN NN GGTNCTCG GTTGTGANT CNACCGNANG CCANGGATTC CNAAGGAAGG      480
TGCGTTNTTG GCCCTACCC TTCGCTNCGG NNCACCTTC CCGACNANGA NCCGCTCCCG      540
CNCNCGNNG CCTCNCCTCG CAACACCCGC NCTCNTNGT NCGGNNCCC CCCCACCCGC      600
NCCCTCNCN NGNCGNANCN CTCNCCNCC GTCTCANNCA CCACCCCGCC CCGCCAGGCC      660
NTCANCCACN GGNNGACNNG NAGCNENNTC GCNCCGCGCN GCGNCCCT CCGCNCNGAA      720
CTNCTCNGG CCANTNNGC TCAANCCNNA CNAACGCCG CTGCGGGGCC CGNAGCGNCC      780
NCCTCCNCGA GTCCTCCCGN CTTCNACCC ANGNNTTCN CGAGGACACN NNACCCGCC      840
NNCANGCGG                                     849
  
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

GCGCAAATA TACTTCGCTC GNACTCGTGC GCCTCGCTNC TCTTTTCCTC CGCAACCATG      60
TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCCAAACT GANTAACACA      120
CACACNCNAN AGANAAATCC NCTGCCTTCC ANAGTANACN ATTGAACNNG AGAACCANGC      180
NGGCGAATCG TAATNAGGCG TGCGCCGCCA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC      240
CTNCCNACCC TACNTCTTCN NAGCTGTCNN ACCCTNGTN CGNACCCCCC NAGGTCGGGA      300
TCGGGTTTNN NNTGACCGNG CNNCCCCTCC CCCCTCCAT NACGANCCNC CCGCACCACC      360
NANNGCNCGC NCCCGNNCT CTTCGCCNCC CTGTCTNTN CCCCTGTNGC CTGGENCNGN      420
ACCGCATTGA CCCTCGCCNN CTNCNNGAAA NCGNANACGT CCGGGTTGNN ANNANCGCTG      480
TGGGNNNGCG TCTGCNCCGC GTTCCTTCN CNNNCTTCCA CCATCTTCNT TACNGGGTCT      540
CCNCGCCNTC TCNNNACNC CCTGGGACGC TNCCTNTGC CCCCCTTAC TCCCCCCTT      600
CGNCGTGNC CGNCCCCACC NTCATTNCA NACGNTCTTC ACAANNNCCT GGNTNNCTCC      660
CNANCNGCN GTCANCCNAG GGAAGGGNGG GGNNCCNNTG NTGACGTTG NGNGANGTC      720
CGAANANTCC TCNCCNTCAN CNCTACCCCT CGGGCGNNCT CTCNGTINCC AACTTANCA      780
NTCTCCCCCG NGNGCNCNTC TCAGCCTCNC CNCCCCNCT CTCTGCANTG TNCCTGCTC      840
TNACCNNTAC GANTNTTCGN CNCCCTCTTT CC                                     872
  
```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATTC	TATAGNGTCA	CCTAAATANC	TTGGCNTAAT	CATGGTCNTA	60
NCTGNCTTCC	TGTGTCAAAT	GTATACNAAN	TANATATGAA	TCINATNTGA	CAAGANNNGTA	120
TCNTNCATTA	GTAACAANTG	TNNTGTCCAT	CCTGTCNGAN	CANATTCCCA	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGGAA	NTCNNNTNNN	NCACCNNCA	CTATCNTNCC	240
GCNCCCTGAC	TGNNAGAGAT	GGATNANTTC	TNNINTGACC	NACATGTTCA	TCTTGGAATTN	300
AANANCCCCC	CGCNGNCCAC	CGGTTNGNNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTGCGTC	AGANNCATCA	AACNTGGGAA	ACCCGCNNCC	ANGTNNAAGT	NGNNNCANAN	420
GATCCCGTCC	AGGNTTNACC	ATCCCTTCNC	AGCGCCCCCT	TTNGTGCCTT	ANAGNGNAGC	480
GTGTCCNANC	CNCTCAACAT	GANACGCGCC	AGNCCANCCG	CAATTNGGCA	CAATGTGCNC	540
GAACCCCTTA	GGGGGANTNA	TNCAAANCCC	CAGGATTGTC	CNCNCANGAA	ATCCCNCAAC	600
CCCNCCCTAC	CCNNCTTTGG	GACNGTGACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCCACCGGT	NNCNTGCGG	GGGTGAANCT	CNGNNTCANC	CNGNCGAGGN	NTCGNAAGGA	720
ACCGGNCCTN	GGNCGAANNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCCTCNCCA	780
NCCNACNGNT	AGNTCCCCCC	CNGGGTNCGG	AANGG			815

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	GCGTACTCCA	AAGATTCAAG	TTTACTCACG	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATTT	CCTGAATTGC	TATGTGTCTG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAAG	TGGAGCATTC	AGACTTGTCT	TTCAGCAAGG	240
ACTGGTCTTT	CTATCTCNTG	TACTACACTG	AATTCACCCC	CACTGAAAAA	GATGAGTATG	300
CCTGCCGTGT	GAACCATGTG	ACTTTGTCAC	AGCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTTTGAAGAT	GCGGCATTTG	GATTGGATGA	ATTCCAAATT	420
CTGCTTGCTT	CNNTTTTAAT	ANTGATATGC	NTATACACCC	TACCCCTTAT	GNCCCCAAAT	480
TGTAGGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAAANT	CCNCCNTTCG	540
AATTGCCCGT	CNCCNGTTN	NGAATGTTTC	CNNAACCACG	GTTGGCTCCC	CCAGGTCNCC	600
TCTTACGGAA	GGGCCTGGGC	CNCTTTNCAA	GGTTGGGGGA	ACCNAAAATT	TCNCTTNTGC	660
CCNCCNCCA	CNNTCTTGNG	NNCNCANTTT	GGAACCCTTC	CNATTCCCCT	TGGCCTCNNA	720
NCCTTNCTA	ANAAAACTTN	AAANCGTNGC	NAAANNTTTN	ACTTCCCCCC	TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs  
 (B) TYPE: nucleic acid



(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

ANATTANTAC AGTGTAACTCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT 60
CCCANAGATA NCTTATANCA ACAGTGCTTT GACCAAGAGC TGCTGGGCAC ATTTCTTGCA 120
GAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCCAGAG GGGTGAGTAG 180
CCATCANGCC TTCGGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA 240
NTGATGACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA 300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC 360
TTCCTACCTG ACNACCAGNG ACCNNNACT GCNGCCTGGG GACAGCNCCTG GGANCAGCTA 420
ACNNAGCACT CACCTGCCCC CCCATGGCCG TNCGCNTCCC TGGTCCTGNC AAGGGAAGCT 480
CCCTGTTGGA ATTNCGGGGA NACCAAGGGA NCCCCCTCCT CCANCTGTGA AGGAAAAANN 540
GATGGAATTT TNCCTTCCG GCCNNTCCC TGTTCCTTTA CACGCCCCCT NNTACTCNTC 600
TCCCTCTNTT NTCCTGNCNC ACTTTTACC CCNNNATTTT CCTTNATTGA TCGGANNCTN 660
GANATTCCAC TNNCGCCTNC CNTCNATCNG NAAANACNAA NACTNTCTNA CCCNGGGGAT 720
GGGNCCCTCG NTCATCCTCT CTTTTTCNT ACCNCCNNTT CTTTGCCTCT CCTTNGATCA 780
TCCAACNCTC GNTGGCCNTN CCCCCCNNT TCCTTTNCCC 820

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

TCTGGGTGAT GGCCTCTTCC TCCTCAGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT 60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTACAGCCTT GCCCAACCTG ATTCTGATGA 120
CTGCGGATGC TGTGACGGAC CCAAGGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGGCG 180
CTGCTGAGCA CTTCCGCCCC TCACCTTGCC CAGCCCTGTC CATGAGCTCT GGGCTGGGTC 240
TCCGCCTCCA GGGTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC 300
TTCTTCTGC CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCTGTGC ANGNCCTTG 360
GATCTCAGTT TCCCTCNCCT ANNGAACTCT GTTCTGANN TCTTCANTTA ACTNTGANTT 420
TATNACCNAN TGGNCTGTNC TGTNNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC 480
NCTCCCTTCC ANTTNMMNNA ACCNGCTTNC CNTCNTCTCC CCNTANCCCG CCNGGGAANC 540
CTCCTTTGCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC 600
CTGNTNNCCC CNCTCNCNNT TNCCTCGTCC CNNCNCGCN NNGCANNTT NCNGTCCCN 660
TNNCTCTCN NGTNTCGNAA NGNTCNCNTN TNNNNNGNCN NGNTNNTN CN TCCCTCTCNC 720
CNNNTGNANG TNNTTNNNNC NCNGNNCCCC NNNNCNNNNN NGGNNTNMMN TCTNCNCNGC 780
CCCNCCCCC NGNATTAAGG CCTCCNNTCT CCGGCCNC 818

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATACG AGNATAANGG GGGAGGTGTG      60
TCCCAACATG ANGGTGNNGT TCTCTTTTGA ANGAGGGTTG NGTTTTTANN CCNGGTGGGT      120
GATTNAACCC CATTGTATGG AGNNAAGGN TTNAGGGAT TTTTCGGCTC TTATCAGTAT      180
NTANATTCCCT GTNAATCGGA AAATNATNTT TCNNCNGGAA AATNTTGCTC CCATCCGNAA      240
ATTINCTCCCG GGTAGTGCAT NTTNGGGGGN CNGCCANGTT TCCCAGGCTG CTANAATCGT      300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG      360
TNNNTTNCCT TCGCCCTNTG ACTCTGCMNG AGCCCAATAC CCNNGNGNAT GTCNCCCNGN      420
NNNGCGNCNC TGAAANNKNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAGCANN      480
CGTTTCNCAT NAAGGCACTT TNGCCTCATC CAACCNCTNG CCCTCNNCCA TTTNGCCGTC      540
NGGTTNCCTT ACGCTNNTNG CNCCTNNNTN GANATTTTNC CCGCCTNGGG NAANCCTCCT      600
GNAATGGGTA GCGNCTTNTC TTTTNACCNN GNGGTNTACT AATCNNCTNC ACGCNTNCTT      660
TCTCNACCCG CCCCCTTTTT CAATCCCAN C GGCNAATGGG GTCTCCCCNN CGANGGGGGG      720
NNNCCANN C C      731

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGNCNC TTCTATGANT ANTNTTAGAT      60
CGCTCANACC TCACANCTC CCNACNANGC CTATAANGAA NANNAAATAGA NCTGTNCNNT      120
ATNTNTACNC TCATANNCTT CNMNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN      180
TNNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC      240
TCNCCATNTN GCCTANANTA NGTNCATACC CTATACCTAC NCCAATGCTA NNNCTAANCN      300
TCCATNANTT ANNNTAACCTA CCACTGACNT NGACTTTTNC ATNANCTCCT AATTGGAATC      360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC      420
NTCAACAACC TATCTANCTG TTCNCCAACC NTINCCCTCCG ATCCCCNNAC AACCCCCCTC      480
CCAAATACCC NCCACCTGAC NCCTAACCCN CACCATCCCG GCAAGCCNAN GGNCATTAN      540
CCACTGGAAT CACNATNGGA NAAAAAAAAC CCNAACTCTC TANCNCNNAT CTCCCTAANA      600
AATNCTCCTN NAATTTACTN NCANTNCCAT CAANCCACN TGAAACNNA CCCCTGTTTT      660
TANATCCCTT CTTTCGAAAA CCNAGCCTTT ANNNCCCAAC CTTTNGGGCC CCCCNCCTNC      720
CCNAATGAAG GNCNCCCAAT CNANGAAACG NCCNTGAAAA ANCNAGGCNA ANANNNTCCG      780
CANATCCTAT CCCTTANTTN GGGGNCCCTT NCCNGGGGCC CC      822

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCAAT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTGCCA	GCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACENCG	GTGGCAGCTC	CAGCTTTTGT	420
TCCCNTTAAT	GAAGGTTAAT	TGCNCGGTTG	GCGTAATCAT	NGGTCANAAC	TNTTTCCTGT	480
GTGAAATTGT	TNTTCCCCTC	NCNATCCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTTCCN	FTCNNGAAAA	CTGTCNTCCC	CTGENTTNT	GAATCGGCCA	CCCCCNNGG	660
AAAAGCGGTT	TGCNTTTTNG	GGGNTCCTT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGNAT	NNNCTCCNC	NAAGGGGNG	AGNNNGNTAT	780
CCCCAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACCAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGAGGCCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCAANATC	CCTACGATTC	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCIT	360
NGCANTTCT	GGCTGTTTAT	GGAAAGCACA	GGTGTCNAT	TINGGCTGGG	ACTTGTGTACA	420
TATGGTTCCG	GCCCACCTCT	CCCNTCNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCINTTG	480
CCTGGGGCCCT	TAANTACCCA	CACCGGAAC	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCCN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCNCTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNNGG	CACNATCCAA	TCCCCCCCCN	TGGGGGCCCC	660
AGCCCAANGG	CCCCGNTCTG	GGNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCAGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCC	CCNNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTNNCCNAG	GGCAGGTTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTNN	AATTTCCACG	GGCACAATGC	GGTCGCANCC	CCTCACCACC	300
NATTAGGAAT	AGTGGTNTTA	CCNCCNCCG	TTGGCNCAC	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCCC	CAAAAAANCN	CCCCAAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGCNCA	NCAGGNCAAC	540
CCAAAGTTC	TTGNGGCCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTTCAA	CAAAGTCATC	600
CCCCTTGGCC	CCCAAATCCT	CCCCCGGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CENNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNACGNC	TANCAANGNA	TCCCTTTTTT	TANAAACGGG	780
CCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTCATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAGTTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGTTTCTGA	CTTTTCAGGA	GTTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTTCAAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTTT	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTTCTCGC	TTCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGCGGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

GCCGCGACCG GCATGTACGA GCAACTCAAG GGCGAGTGGG ACCGTAAAAG CCCCAATCTT      60
ANCAAGTGGC GGAAGAGCT GGGTCGACTC AAGCTAGTTC TTCTGGAGCT CAACTTCTTG      120
CCAACCACAG GGACCAAGCT GACCAAACAG CAGCTAATTC TGGCCCGTGA CATACTGGAG      180
ATCGGGGGCCC AATGGAGCAT CCTACGCAAN GACATCCCCT CCTTCGAGCG CTACATGGCC      240
CAGCTCAAAT GCTACTACTT TGATTACAAN GAGCAGCTCC CCGAGTCAGC CTATATGCAC      300
CAGCTCTTGG GCCTCAACCT CCTCTTCCTG CTGTCCGAGA ACCGGGTGGC TGANTNCCAC      360
ACGGANTTGG ANCGGCTGCC TGCCCAANGA CATAANACC AATGTCTACA TCNACCACCA      420
GTGTCCTGGA GCAATACTGA TGGANGGCAG CTACCNCAAA GTNTTCCTGG CCNAGGGTAA      480
CATCCCCCGC CGAGAGCTAC ACCTTCTTCA TTGACATCCT GCTCGACACT ATCAGGGATG      540
AAAATCGCNG GGTGCTCCA GAAAGGCTNC AANAANATCC TTTCNCTGA AGGCCCCCGG      600
ATNCNCTAGT NCTAGAATCG GCCCGCATG GCGGTGGANC CTCCAACCTT TCGTTNCCCT      660
TTACTGAGGG TTNATTGCCG CCCTTGGGGT TATCATGGTC ACNCCNGTTC CCTGTGTTGA      720
AATTNTTAAC CCCCCACAAT TCCAGGCCNA CATTTG

```

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GGGGATCTCT ANATCNACCT GNATGCATGG TTGTCGGTGT GGTCGCTGTC GATGAANATG      60
AACAGGATCT TGCCCTTGAA GCTCTCGGCT GCTGTNTTGA AGTTGCTCAG TCTGCCGTCA      120
TAGTCAGACA CNCTCTTGGG CAAAPAAACAN CAGGATNTGA GTCTTGATTT CACCTCCAAT      180
AATCTTCNCG GCTGTCTGCT CGGTGAACCTC GATGACNANG GGCAGCTGGT TGTGTNTGAT      240
AAANTCCANC ANGTTCTCCT TGGTGACCTC CCCTTCAAAG TTGTTCCGGC CTTCATCAAA      300
CTTCTNNAAN ANGANNANCC CANCTTTGTC GAGCTGGNAT TTGGANAACA CGTCACTGTT      360
GGAAACTGAT CCCAAATGGT ATGTCATCCA TCGCCTCTGC TGCCCTGCAA AAACCTTGCTT      420
GCCNCAAATC CGACTCCCN TCCTTGAAAG AAGCCNATCA CACCCCTCCT CCTGGACTCC      480
NNCAANGACT CTNCCGCTNC CCCNTCCNNG CAGGGTTGGT GGCANNCCGG GCCNTGCGC      540
TTCTTCAGCC AGTTCACNAT NTTATCAGC CCCTCTGCCA GCTGTNTAT TCCTTGGGGG      600
GGAANCCGTC TCTCCCTTCC TGAANNAACT TTGACCGTNG GAATAGCCGC GCNTCNCCNT      660
ACNTNCTGGG CCGGGTTCAA ANTCCCTCCN TTGNCNNTCN CCTCGGGCCA TTCTGGATT      720
NCCNAACCTT TTCCTTCCC CNCCCNCCG NGTTTGGNTT TTTATNGGG CCCCCAATCT      780
GCTNTTGGCC ANTCCCTGG GGGCNTNTAN CNCCCTNTT GGTCCCNTNG GCCC      834

```

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCGNCGCTTT	CCNGCCGCGC	CCCGTTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCTGTGA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTTT	ETTCTCATGG	CTGCCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTTG	GANAAATATT	CTTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTTCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTGTG	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGGANGTC	NTTNCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCTGAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCTT	GGGTCCANT	CCCTCCTTTG	TINCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCTCAAA	GTGTCTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTGTAGTAGT	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTTG	TCACTGGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTACACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCTGCAC	ACTCCACTAA	ACTGTCGATN	CANCAGCCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGGAAAT	360
CNCCTNANCC	CAAAGTGCCT	CTCAAAGGCC	ACCTTGACAC	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CAAAGGTAG	TTGTTCCTTG	TGCCCAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAAATC	TGCTCCGTGG	GGGTCAATNN	TACCANGGTT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCCT	GTITGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTTAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCTTGAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNTTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATTT	CCGGGGGGGG	GTTCCAAACC	120

CAAATTAATT TTGGANTTTA AATTAAATNT TNATTTNGGGG AANAANCCAA ATGTNAAGAA 180  
 AATTTAATCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTTTAAACC 240  
 CTTAAATCCC TCCGAAATTG NTAANGGAAA ACCAAATTCN CCTAAGGCTN TTTGAAGGTT 300  
 NGATTTAAAC CCCCTTNANT TTTTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGTIT 360  
 TCCINTTAAN CNTNGGTAAC TCCCGNTAAT GAANNNCCCT AANCCAATTA AACCGAATTT 420  
 TTTTGAATT GGAAATTCN NGGGAATTNA CCGGGGTTTT TCCNNTTGG GGGCCATNCC 480  
 CCCNCTTTTCG GGGTTTGGN NTAGGTTGAA TTTTNNANG NCCCAAAAAA NCCCCAANA 540  
 AAAAACTCC CAAGNNTTAA TTNGAATNTC CCCCTTCCA GGCCTTTTG GAAAGNGGG 600  
 TTTNTGGGGG CCNGGGANTT CNTTCCCCCN TTNCCNCCC CCCCCNGGT AAANGGTTAT 660  
 NGNNTTGGT TTTTGGGCC CTTNANGGAC CTTCGGGATN GAAATTAAT CCCCCGGNCG 720  
 GCCG 724

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTCTTTG CTCACATTTA ATTTTATTT TGATTTTTTT TAATGCTGCA 60  
 CAACACAATA TTTATTTTAT TTGTTTCTTT TATTTTCAAT TATTTGTTTG CTGCTGCTGT 120  
 TTTATTTTAT TTTACTGAAA GTGAGAGGGA ACTTTTGTGG CCTTTTTTCC TTTTCTGTA 180  
 GGCCGCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT 240  
 CGCAAATCA CTCGGGGGAA NGGAAAGGTT GCTTTGTAA TCAATGCCCTA TGGTGGGTGA 300  
 TTAAGTCTT GTACAATTAC NTTTTCACTT TAATTAATTG TGCTNAANGC TTTAATTANA 360  
 CTGCGGGGTT CCCTCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG 420  
 TCCCGGCNNT CNTTGAAACA CACNGCNGAA NGTTCTCATT NTCCCNCCN CAGGTNAAAA 480  
 TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCNNN GCCTGAATCC TCNAAAANCN 540  
 CCCTCAANCN AATTNCTNNG CCGGGTCNC GCNTNNGTCC CNCCCGGGCT CCGGGAANTN 600  
 CACCCCNCA ANNCNNTNNC NAACNAAAT CCGAAAATAT TCCCNNTCNC TCAATTCCCC 660  
 CNNAGACTNT CCTCNNCNAN CNCAATTTT TTTTNTTAC GAACNCGNNC CNNAAAATGN 720  
 NNNNCNCCTC CNCTNGTCCN NAATCNCCAN 751

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTTT CTGTAAGATC AGGTGTTCTT CCCTCGTAGG TTTAGAGGAA ACACCCTCAT 60  
 AGATGAAAC CCCCCGAGA CAGCAGACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG 120  
 CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA 180  
 TGGTCTGGAA GCGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAAT 240  
 TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGGT 300

```

CGGTCATAAN CGCGGTGGCG TCGTCGCTGG GAGCTGGCAG GGCCTCCCGC AGGAAGGGNA      360
ATAAAAGGTG CGCCCCCGCA CCGTTCANCT CGCACTTCTC NAANACCATG ANGTTGGGCT      420
CNAACCCACC ACCANNCCGG ACTTCCTTGA NGGAATTCCC AAATCTCTTC GNTCTTGGGC      480
TTCTNCTGAT GCCCTANCTG GTTGCCCNNG ATGCCAANCA NCCCCAANCC CCGGGGTCTCT      540
AAANCACCCN CCTCCTCNTT TCATCTGGGT TTTTNTCCCC GGACCNTGGT TCCTCTCAAG      600
GGANCCCATATA TCTCNACCAN TACTCACCNNT NCCCCCCCNT GNNACCCANC CTTCTANNGN      660
TTCCNCCCCG NCCTCTGGCC CNTCAAANAN GCTTNCACNA CCTGGGTCTG CCTTCCCCCC      720
TNCCCTATCT GNACCCCN CN TTTGTCTCAN TTT      753

```

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG      60
AGTGAACCCA TCCTTGATTT ATATACATAT ATGTTCTCAG TATTTGGGA GCCTTTCCAC      120
TTCTTTAAAC CTTGTTTATT ATGAACACTG AAAATAGGAA TTTGTGAAGA GTTAAAAAGT      180
TATAGCTTGT TTACGTAGTA AGTTTTTGAA GTCTACATTG AATCCAGACA CTTAGTTGAG      240
TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTTCAGAG GTATTTTCAT      300
TTTTACTTTT TGATTAATTG TGTTTTATAT ATTAGGGTAG T      341

```

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTTAGTGT TGTATCATAA ATACTTTGAT      60
GTTTCAAACA TTCTAAATAA ATAATTTTCA GTGGCTTCAT A      101

```

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC      60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT      120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA      180
CCTCTTGAGA GGTCACTAAA GAGGACTTAA TATTTTATAT CTACAAAATG ACCACAGGAT      240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC      300
TCGAA                                     305

```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTTCCT      60
GATTATTTGG TGTGTGTTT GGTGTTGTGC CAAAGTATTG GCAGCTTCAG TTTTCATTTT      120
CTCTCCATCC TCGGGCATTG TCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT      180
CCAGAATTTT TCTTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC      240
TGCTGTTGTT CTTCTTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTT AAGAACCTGA      300
AGACGCCCTC AGATCGGTCT TCCCATTTTA TTAATCCTGG GTTCTTGCTT GGGTTCAAGA      360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC      420
ACTTGGCAGG GGGGTCTTGC TCCTTTTTC TATCAGGTGA CTCTGCAACA GGAAGGTGAC      480
TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTT GCTGTCCAAC AAATCTACTG      540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTT ATGATGGAAG      600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC      660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG      720
CCGCCCGGGT GAACTCCTGC AAATCATGCT TGCAAAGGTG CTCGCCGTTG ATGTCGAACT      780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTGTTGTTC CAGGAGGTGA TGGAGCCACT      840
CCACACCTG GT                                     852

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTGCGAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTTATT TAAATGTTTA TAAAGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cdNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTCTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGGA GGTTCAGAC	120

GCTTCACTGC	TTGAAACTTA	AATGGATGTG	GGACANAATT	TTCTGTAATG	ACCCTGAGGG	180
CATTACAGAC	GGGACTCTGG	GAGGAAGGAT	AAACAGAAAG	GGGACAAAGG	CTAATCCCAA	240
AACATCAAAG	AAAGGAAGGT	GGCGTCATAC	CTCCCAGCCT	ACACAGTTCT	CCAGGGCTCT	300
CCTCATCCCT	GGAGGACGAC	AGTGGAGGAA	CAACTGACCA	TGTCCCCAGG	CTCCTGTGTG	360
CTGGCTCCTG	GTCTTCAGCC	CCCAGCTCTG	GAAGCCCACC	CTCTGCTGAT	CCTGCGTGGC	420
CCCACTCCT	TGAACACACA	TCCCCAGGTT	ATATTCTTGG	ACATGGCTGA	ACCTCCTATT	480
CCTACTTCCG	AGATGCCTTG	CTCCCTGCAG	CCTGTCAAAA	TCCCCTCAC	CCTCCAAACC	540
ACGGCATGGG	AAGCCTTTCT	GACTTGCCTG	ATTACTCCAG	CATCTTGGAA	CAATCCCTGA	600
TTCCCCACTC	CTTAGAGGCA	AGATAGGGTG	GTTAAGAGTA	GGGCTGGACC	ACTTGGAGCC	660
AGGCTGCTGG	CTTCAAATTN	TGGCTCATT	ACGAGCTATG	GGACCTTGGG	CAAGTNATCT	720
TCATTCTAT	GGGCNTCATT	TTGTTCTACC	TGCAAAATGG	GGGATAATAA	TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT 60  
 TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTTT AATTACAGCT CAACGCAACT 120  
 TGGT

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA	CTATTTTATT	GCAGGAGGTG	GGGGTGTTTT	TATTATTCTC	TCAACAGCTT	60
TGTGGCTACA	GGTGGTGTCT	GACTGCATNA	AAAANTTTTT	TACGGGTGAT	TGCAAAATTT	120
TTAGGGCACC	CATATCCCAA	GCANTGT				147

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC      60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT      107
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG      60
CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG      120
GCCTTGCAAG GTCAGAAAGG GGA CT CAGGG CTTCCACCAC AGCCCTGCCC CACTTGGCCA      180
CCTCCCTTTT GGGACCAGCA ATGT      204
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA      60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA      120
CCATCAGACA GGTTTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA      180
AAACTTCTT GTATCAATTT CTTTGTGTTCA AAATGACTGA CTTAANTATT TTAAATATT      240
TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA      300
ATGTTGCTCA GATAATAAAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTTCTGGGCG      360
ATGCAACAGT GTCTTTTCTT TNCTTTTTTCT TTTTTTTTTT TTACAGGCAC AGAAACTCAT      420
```

CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT 480  
ATCACTCTTG T 491

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTN TATGATCTGA 60  
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTGG CTTTGATAAC 120  
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAAC ATTAGCTGCT 180  
CAATCAAATC TCTACATAAC ACTATAGTAA TTAACACGTT AAAAAAAGT GTTGAAATCT 240  
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC 300  
AGCTTTGANT TTCCTTGTGC TGATANGAGG AAAGGCTGAA TTACCTPGTT GCCTCTCCCT 360  
AATGATTGGC AGGTCNGGTA AATNCCAAA CATATTCCAA CTCAACACTT CTTTCCNCG 420  
TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTTT 480  
CANT 484

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAACGGTG CCATCCCTGA ACACGGCTGG 60  
CCACTGGGTA TACTGCTGAC AACCGCAACA AAAAAACAC AAATCCTTGG CACTGGCTAG 120  
TCTATGTCCT CTCAAGTGCC TTTTGTGTTG T 151

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCACGG TCCCCAGAAC GGACACTTTC 60  
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T 91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT 60  
TGGATTTTGT GTATCTGTGG GTTGGGGGGA CCGTCCAGGA ACCAATACCC CATGGATACC 120  
AAGGGACAAC TGT 133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC 60  
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA 120  
TCTCANTGGG CTGGATNCAT GCAGGGT 147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAAATAC ATTGAATTTT CTGTATACTC 60
TGATTACATA CATTTATCCT TTAAAAAAGA TGAAATCTT AATTTTATG CCATCTATTA 120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAGTAGTT 180
TTGACTTCTA AGTTTGGT 198
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAACTG GTGATGGCTA CTGAAAAGAT 60
CCATTGAAAA TTATCATTA TGATTTTAAA TGACAAGTTA TCAAAAACCTC ACTCAATTTT 120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA 180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG 240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT 300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT 330
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC 60
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC 120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT 175
```

(2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT      60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC      120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT                                     154
```

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
CGCTCGAGCC CTATAGTGAG TCGTATTAGA                                     30
```

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
ACAAGTCATT TCAGCACCCT TTGCTCTTCA AAAGTGACCA TCTTTTATAT TTAATGCTTC      60
CTGTATGAAT AAAAATGGTT ATGTCAAGT                                     89
```

## (2) INFORMATION FOR SEQ ID NO:64:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCCTGCAG 60  
 AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT 97

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCT TTTGATGGCA 60  
 GCATGGCGTC CTAGGCCTTG ACACAGCGGG TGGGGTTTGG GCTNTCCCAA ACCGCACACC 120  
 CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT 180  
 TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA 240  
 GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG 300  
 TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG 360  
 GGGCGGGAGG AGCATGT 377

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG 60

AGAACCCGTG	TGCCCCCTTCC	CACCATATCC	ACCCTCGCTC	CATCTTTGAA	CTCAAACACG	120
AGGAACCTAAC	TGCACCCTGG	TCCTCTCCCC	AGTCCCCAGT	TCACCCTCCA	TCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCTGAATT	TATGTGGTTT	240
TTATATATTT	TTTAATAAGA	TGCACTTTAT	GTCATTTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACCTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTTAAA	AAAGGGGACT	TGCTTAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCTGATCTC	AGCACTCCTT	AGTCTGCTTG	300
CTCTCTCCAG	GGCCCCAGCC	TGGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTTCT	GTGCTAGTGG	ACCGT				385

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG	ATATATTTTT	ACCCAGATG	GCGATATTCT	TTGTAAAAAA	TGAAAATAAA	60
GTATTTTTTAA	TGG					73

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGGCCGAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGCCCG AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCTTCACCTT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCCAA CTTGGACACC TGTGCCTTCC ATGAACAGCC	420
AGAAGTGCAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCTT GGGGAGAACA	480
GAANGTCCCT GGGTGAAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCAA GGCCACCACA CACCACCTGT	180
CCAAAAAGGC CTTGATACG GGATAATCCT ATTTATTACC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCCC AACAGGCATC ACCCCGCTAA ATCCCCTAGA AGTCCCACTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATTT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTTCTACAT	AGATAGTACT	60
AGGTATTAA	AGATATGTAA	AGAAAGAAAT	CACACCATTA	ATAATGGTAA	GATTGGTTTA	120
TGTGATTTTA	GTGGTATTTT	TGGCACCCTT	ATATATGTTT	TCCAAACTTT	CAGCAGTGAT	180
ATTATTTCCA	TAACTTAAAA	AGTGAGTTTG	AAAAAGAAAA	TCTCCAGCAA	GCATCTCATT	240
TAAATAAAGG	TTTGTCTACT	TTAAAAATAC	AGCAATATGT	GACTTTTTTA	AAAAGCTGTC	300
AAATAGGTGT	GACCCTACTA	ATAATTATTA	GAAATACATT	TAAAAACATC	GAGTACCTCA	360
AGTCAGTTTG	CCTTGAAAAA	TATCAAATAT	AACTCTTAGA	GAAATGTACA	TAAAAGAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTTCCCTC	CTCAATTTTG	TATTTTAAAA	AAGTACATGG	480
TAAAAAATAA	AATTCACAAC	AGTATATAAG	GCTGTAAAAA	GAAGAATTCT	GCC	533

## (2) INFORMATION FOR SEQ ID NO:72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	TAAAGAACAC	TAAAAGAGGG	ACAAGGCTAA	120
AAGCCGAGG	ATGTCTACAC	TATANCAGGC	GCTATTTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCCAC	TGGTTTGAAA	ACCGTTCCTC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCCC	GTCTGTTATG	420
ATTTCTCTCC	ATTGCAGCNA	NAAACCCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACCNGGAGG	A			511

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCACTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTGG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCCAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	180
CAAGTGAGAT	TTTAGATATT	GTTAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	240

CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA 300  
 CTCTGCATTA AATCTATTG CCATTTCCTGA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCG 360  
 ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTGGCCAGC 420  
 CATCTGTTGT TFGCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCCT 480  
 GTCCTTTCCT AANTAAAT 499

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTT GGATTCAGCC GCGAAGAGAT 60  
 TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT 120  
 TCCAGGCCCA CGGCTCAAGT GAATTGAAT ACTGCATTGA CAGTGTAGAG TAACACATAA 180  
 CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCTTACCACT CTAATCAAGA 240  
 AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG 300  
 GGCTTTTGAT TTATAANACT TTGGGTACTT ATACTAAAATT ATGGTAGTTA TACTGCCTTC 360  
 CAGTTTGCTT GATATATTTG TTGATATTAA GATTCTTGAC TTATATTTG AATGGGTTCT 420  
 ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTATTTA CACTCTTGAT 480  
 TCTACAATGT AGAAAATGAA GGAAATGCCC CAAATTGTAT GGTGATAAAA GTCCCGT 537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACTACTCTG CTGCAGCTCA CAAACACCTC 60  
 TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA 120  
 CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG 180  
 TGGCACAAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAAGCGT CTCTGAGGA 240  
 TCTAGTTGGG CTTTCTTTCT GGGTTTGGGC CATTTCANIT CTCATGTGTG TACTATTCTA 300  
 TCATTATTGT ATAACGGTTT TCAAACCNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA 360  
 CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTINT TCCAGAGCTC 420  
 CTCCAGCCAA CCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN 467

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTCTGGGC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTCAGGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTTCC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAGTG	GAGCATTCAG	240
ACTTGTCTTT	CAGCAAGGAC	TGGTCTTTCT	ATCTCTTGTA	CTACACTGAA	TTCAACCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTTC	AAGCCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCCC	CGGCGGGGA	TGCGAGGCTC	GGAGCACCCT	TGCCCGGCTG	TGATTGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTTCTGTCC	CTTTGCTCCC	GGCAAGCGCT	TCTGCTGAAA	180
GTTTCATATCT	GGAGCCTGAT	GTCTTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
AAAAAAA						248

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA	60
TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTT ATAAATGCCT	180
GATTTAAAAA AAAAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 552 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTTGTT AGGTTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCCT ATTCTTTATT	120
CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATFGAGGT GGATAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTAGTTT AATATGCTGT TGAACCTACT	300
CTGTTTCCTT GCTAGAAAAA ATTATAAACA GGACTTTGTT AGTTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGAATTTT	420
TTCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTTGGT TAATACGTTA ATATGTCTN AATNAACAAG GCNTGACTTA TTTCCAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATT T GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTCACG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTAAACT TTCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300

TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAATGTT CTGGTTTCNC TTAAAAAAA AAAAAAAA AAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTCTCCTA CAAGTGAGAT TTTAGATATT	240
GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTG	360
CCATTTCAAA AAAAAAAAAA AAA	383

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAACTCT TCGGACTGTG	300
AGCCCTGATG CCTTTTGTCC AGCCATACTC TTGGCCTCC AGTCTCTCGT GGGGATTGAT	360
TATGCTTGTTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGAACACAT TTGANTTTTT	420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCTC CTGGGGCCCA GGCGGGCACC TGCCTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTTCA TTACACATTC GGCAAGTAC AGGGCAACAG CNATCTCTAC TGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA      240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNNGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNGC GCNTNCCTTT      480
T

```

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCATT      60
ACTTGGA AAA GCAACTTNA GCCTGGACAC TGGTATTAAA ATTCACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCATCACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTAC ACCTGT TAAA AGGGCGCTAA GCATTTTTGA TTCAACATCT TTTTTTTGA      240
CACAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACTTTCTT      300
CATGGGACAG AGCCATTGA TTTAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTINACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG      472

```

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

AGAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG      60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG      120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT      180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT      240
TTTATTTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG      300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA      360

```

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTTT TTT

413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCCTCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCGCTG CTCCTGCTGG CCATCCTGGC	120
CGTGCCCTG GCCGTGAGCC CCGCGGCCG CTCCAGTCCC GGCAAGCCGC CGCGCTGGT	180
GGGAGGCCCA TGGACCCCGC GTGGAAGAAG AAGGTGTGCG GCGTGACTG GACTTTGCCG	240
TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCG	300
CCCAANCAAA TTGTTACTNG GGGTAANTAA TTCTTGGAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAGAA CCNAGCCAAT TNGAACAAAT NCCCTCCAT AACAGCCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTTC CAAATTTT	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTC TGCCAAAGTT GGTGTTGTAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNTTCT GATGCGAAGT TCTNATTCCA GTGTTTTAGT CTTTGCATC	240
TTTNAATGTTN AGACTTGCCT CTNTNAAATT GCTTTTGENT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTGTA ATATCTTACA TCTNAAAATN	360
AATCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN	420
AATTCNNANA ANTTCAGTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGTTTCANCCA CCAACTCTAC AAGTTGCTGT	60
CTTCCACTCA CTGTCTGTAA GCNTNTTAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT	120
TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTGAG TTAGTATAAG CTCTTCCACT	180
TCCTTTGTTA AGACTTCATC TGGTAAAGTC TTAAGTTTGT TAGAAAGGAA TTTAATTGCT	240
CGTTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCCT	300
TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTTA AATTCTGCAA	360
GAGTCATCTG TCTGCAAAAG TTGCGTTAGT ATATCTGCCA	400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC	120
ATGCCTCTTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTCTT	180
TGTGGAAAAA CTGGCACTTG NCTGGAAC TA GCAAGACATC ACTTACAAAT TCACCCACGA	240
GACACTTGAA AGGTGTAACA AAGCGACTCT TGCATTGCTT TTTGTCCCTC CGGCACCAGT	300
TGTCAATACT AACCCGCTGG TTTGCCTCCA TCACATTTGT GATCTGTAGC TCTGGATACA	360
TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAA AGCAACTCTT GGTGCCTGTT	420
NGATCAGGTT CCCATTTCCT AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCA NATCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGCGGTCACT 60  
 GGTCCCCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCCTT 120  
 CCCACGCAGG CAGCAGCGGG GCCGGTCAAT GAACTCCACT CGTGGCTTGG GGTGACGGT 180  
 TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCCCGACT GTGCGGGACC 240  
 TGCAGCGAAA CTCCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCAGG GCCTTGCCCA 300  
 GAACCTTCCG CTTGTTCTCT GCGTCACTT GCAGCTGCTG CCGCTNACAC TCGGCTCGG 360  
 ACCAGCGGAC AAACGGCGTT GAACAGCCGC ACCTCACGGA TGCCANTGT GTCGCGCTCC 420  
 AGGAACGGCN CCAGCGTGTC CAGGTCAATG TCGGTGAANC CTCGCGGGT AATGGCG 477

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG ACCTTGCCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC 60  
 AGTCCGAGCA GCCCCAGACC GCTGCCGCCC GAAGCTAAGC CTGCCTCTGG CCTTCCCTC 120  
 CGCCTCAATG CAGAACCANT AGTGGGAGCA CTGTGTTTAG AGTTAAGAGT GAACACTGTN 180  
 TGATTTTACT TGGGAATTTC CTCTGTTATA TAGCTTTTCC CAATGCTAAT TTCCAAACAA 240  
 CAACAACAAA ATAACATGTT TGCCTGTTNA GTTGATAAAA AGTANGTGAT TCTGTATNTA 300  
 AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTTATTGG TNCTCTGGAA 360  
 ATAAATATAT TATTAAA 377

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG GGTTAGGGTC CAGTTCCTCAG TGGAAGAAAC AGGCCAGGAG AANTGCGTGC 60  
 CGAGCTGANG CAGATTTCCC ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT 120  
 CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG 180  
 GAAGGCCCCA TTCCGGGGCT GTTCCCCGAG GAGGAAGGGA AGGGGCTCTG TGTGCCCCC 240  
 ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCTT CACGTGTATC CCCACACAA 300

TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAAG	GGGCAGAATC	TCCAATAGAN	GGANNGAACC	CTTGCTNANA	480
AAAAAAAAANA	AAAAA					495

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATTTT	120
TAGCTGTTTT	GAGTTGATTC	GCACCACTGC	ACCACAACCTC	AATATGAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTGAAAA	GTATACAATG	AAAAATTTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAAA	TGTGGAGTGT	ATGTTCTTTT	CACAGTAATA	TATGCCTTTT	GTAACCTTAC	360
TTGGTTATTT	TATTGTAAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTTCTTT	CCTTGTTTAC	GTTAATTTTG	AAAAGAATGC	AT	472

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAAT	TTCAAAATTA	TATGTAACCT	CTACTAGTTT	TACTTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAGTCTTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAAT	300
TGTGTTAGTC	TCAATTCCTA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACT AGAATGGATA 60  
 AAATAATGCT GCAAACCTTAA TGTTCTTATG CAAATGGAA CGCTAATGAA ACACAGCTTA 120  
 CAATCGCAA TCAAACTCA CAAGTGCTCA TCTGTTGTAG ATTTAGTGTA ATAAGACTTA 180  
 GATTGTGCTC CTTGCGATAT GATTGTTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT 240  
 CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT 300  
 GTGATTATNA AATTAATCAC AAATTTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT 360  
 NTNNTTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG 420  
 TTCNATCTTA TTTTTCCTCCN GACNACTANT TNCTTTTCTTA GGGNCTATTC TGANCCATC 479

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTTGT GGCACTGACA ATCAGACCTA 60  
 TGCTAGTTCC TGTCTATCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA 120  
 TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA 180  
 AGTGATTCAG TTTCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA 240  
 TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACA GAGAAATAAA GTCAGAAAAT 300  
 TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCAT TGAACCTTCT CTTAAGGACT 360  
 TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC 420  
 TTTGGAATAA TCTTGACGGT CCTGAACCTG CTCCTCTGCGA 461

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCCT	60
CGGCGCCTCT GCGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCCT	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCGTGCC TTGGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCTCGGG AAGGGCGGCC	240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC	269

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTTTCAG GTCAACTTCC TTGTCTGTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GGTTCCTTGC CAAATCCAAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTC TCATATCGGT GGCCA	405

## (2) INFORMATION FOR SEQ ID NO:102:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT      60
GGCACTTAAT CCATTTTATAT TCAAAATGT CTACAAATTT AATGCCATTA TACGGTATTT      120
TCAAAATCTA AATTATTCAA ATTAGCCAAA TCCTTACCAA ATAATACCCA AAAATCAAAA      180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA ATATATACGG CTGGTGTTTT      240
CAAAGTACAA TTATCTTAAC ACTGCAAACA TTTTAAGGAA CTAAAATAAA AAAAAACACT      300
CCGCAAAGGT TAAAGGGAAC AACAAATCT TTTACAACAC CATTATAAAA ATCATATCTC      360
AAATCTTAGG GGAATATATA CTTACACGG GATCTTAACT TTTACTCACT TTGTTTATTT      420
TTTTAAACCA TTGTTTGGGC CCAACACAAT GGAATCCCC CTGGACTAGT      470

```

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTTACT      60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC      120
TAAATGGAAA CTGCCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCTTAAAGT      180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTGTGAAAAC ATCCAAATTC      240
ATTTTCTTGT TCTTTAAAAT TATCTAATCT TTCCATTTTT TCCCTATTCC AAGTCAATTT      300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA      360
AGGGAAAACA GGAAGAGAAA TGGCACACAA AACAAACATT TTATATTTCAT ATTTCTACCT      420
ACGTTAATAA AATAGCATTT TGTGAAGCCA GCTCAAAAGA AGGCTTAGAT CCTTTTATGT      480
CCATTTTAGT CACTAAACGA TATCAAAGTG CCAGAATGCA AAAGGTTTGT GAACATTTAT      540
TCAAAAGCTA ATATAAGATA TTTCACATAC TCATCTTTCT G      581

```

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

TTTTTTTTTT TTTTTTTTTT TTTTCTCTTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT 60
CACTCTCTAG ATAGGGCATG AAGAAAACCTC ATCTTTCCAG CTTTAAAATA ACAATCAAAT 120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCTTAT CTCTCCTGA 180
AGGAAATCTG TTCATTCTTC TCATTCTAT AGTTATATCA AGTACTACCT TGCATATTGA 240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT 300
TTCATGCAAA CTAGAAAATA ATGTTTCTTT TGCATAAGAG AAGAGAACAA TATAGCATTAT 360
CAAAACTGCT CAAATGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC 420
AAATCACATT TACGACAGCA ATAATAAAC TGAAGTACCA GTTAAATATC CAAAATAATT 480
AAAGGAACAT TTTAGCCTG GGTATAATTA GCTAATTCAC TTTACAAGCA TTTATTAGAA 540
TGAATTCACA TGTTATTATT CCTAGCCCAA CACAATGG 578

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

TTTTTTTTTT TTTTTCAGTA ATAATCAGAA CAATATTTT TTTTATATT AAAATTCATA 60
GAAAAGTGCC TTACATTTAA TAAAAGTTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT 120
GTCTTGAACA CCAATATTAA TTTGAGGAAA ATACACCAA ATACATTAAG TAAATTATTT 180
AAGATCATAG AGCTTGTAAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTAA 240
AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTTAATTTTG TGATGAATAT 300
GGGGTGTCAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA 360
TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTTCT CTTTCTTCAA TCTTTTAAGG 420
GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTTCTA TGGAAGGATT 480
AGATATGTTT CCTTTGCCAA TATTAAAAAA ATAATAATGT TTACTACTAG TGAAACCC 538

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

TTTTTTTTTT TTTTATAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTTC      60
ATTTATTAGC TCTGCAACTT ACATATTTAA ATTAAAGAAA CGTTTATAGAC AACTGTACAA      120
TTTATAAATG TAAGGTGCCA TTATTGAGTA ATATATTCTT CCAAGAGTGG ATGTGTCCCT      180
TCTCCCACCA ACTAATGAAC AGCAACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT      240
GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG      300
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAAT      360
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCTTC GGTGGCAAGA ACTCTTCGAA      420
CCGCTTCCTC AAAGGCGCTG CCACATTTGT GGCTCTTTGC AGTTGTTTCA AAA      473

```

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

CGCCATGGCA CTGCAGGGCA TCTCGGTCAT GGAGCTGTCC GGCCTGGCCC CGGGCCCGTT      60
CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGGACC GGCCCGGCTC      120
CCGCTACGAC GTGAGCCGCT TGGGCCGGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA      180
GCCGCGGGGA GCCGCCGTGC TGCGGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC      240
CTTCCGCCGC GGTGTCTATG AGAAACTCCA GCTGGGGCCA GAGATTCTGC AGCGGGAAAA      300
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTTGGCCAG TCAGGAAGCT TCTGCCGGTT      360
AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAGGTGTT CTCTCAAAA TTGGCAGAAG      420
TGGTGAGAA CTGATGCCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT      480
GTGTGCAC TGCAATTATA TGGCTCTTT TGACCGCACA CGCACTGACA AGGTCAGGT      540
CATTGATGCA AATATGGTGG AAGGAACAG ATATTAAAGT TCTTTTCTGT GGAAAACTCA      600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT      660
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGAGCAA TAGAACCCCA      720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTC CCAATCAGAT      780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTAATTG CAAAGAAGAC      840
GAAGGCAGAG TGGTGTCAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC      900
TTTTGAGGAG GTTGTTCATC ATGATCACA CAAGGAACGG GGCTCGTTTA TCACCAGTGA      960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCA CCATCCCTTC      1020
TTTCAAAAGG GATCCTTTCA TAGGAGAACA CACTGAGGAG ATACTTGAAG AATTTGGATT      1080
CAGCCGCGAA GAGATTTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA      1140
AGCTAGTCTC TAACCTCCAG GCCCAGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG      1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTTA      1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCATAA      1320
AATGGTTATC ATTAGGGCTT TTGATTTATA AAACCTTGGG TACTTATACT AAATTATGGT      1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTC TTGACTTATA      1440
TTTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATTT      1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGTAT      1560

```

AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620  
A 1621

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro  
1 5 10 15  
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val  
20 25 30  
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg  
35 40 45  
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala  
50 55 60  
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe  
65 70 75 80  
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln  
85 90 95  
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln  
100 105 110  
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala  
115 120 125  
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr  
130 135 140  
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys  
145 150 155 160  
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys  
165 170 175  
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser  
180 185 190  
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg  
195 200 205  
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
210 215 220  
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe  
225 230 235 240  
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
245 250 255  
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala  
260 265 270  
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
275 280 285  
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

290                      295                      300  
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu  
 305                      310                      315                      320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
                     325                      330                      335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
                     340                      345                      350  
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
                     355                      360                      365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
                     370                      375                      380

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC TGC GCCAGGG CCTGAGCGGA GGC GGGGGCA GCCTCGCCAG CGGGGGCCCC 60  
 GGGCCTGGCC ATGCCTCACT GAGCCAGCGC CTGCGCCTCT ACCTCGCCGA CAGCTGGAAC 120  
 CAGTGCAGCC TAGTGGCTCT CACCTGCTTC CTCCTGGGCG TGGGCTGCCG GCTGACCCCG 180  
 GGTTTGATCC ACCGCGGCCG CACTGTCCTC TGCATCGACT TCATGGTTTT CACGGTGCGG 240  
 CTGCTTCACA TCTTCACGGT CAACAAACAG CTGGGGCCCA AGATCGTCAT CGTGAGCAAG 300  
 ATGATGAAGG ACGTGTCTTT CTTCTCTTTC TTCTCGGCG TGTGGCTGGT AGCCTATGGC 360  
 GTGGCCACGG AGGGGCTCCT GAGGCCACGG GACAGTACT TCCCAAGTAT CCTGCGCCGC 420  
 GTCTTCTACC GTCCCTACCT GCAGATCTTC GGCAGATTG CCCAGGAGGA CATGGACGTG 480  
 GCCCTCATGG AGCACAGCAA CTGCTCGTCG GAGCCCGGCT TCTGGGCACA CCCTCCTGGG 540  
 GCCCAGGCGG GCACCTGCGT CTCCAGTAT GCCAACTGGC TGGTGGTGCT GCTCCTC3TG 600  
 ATCTTCTGTC TCGTGGCCAA CATCCTGCTG GTCAACTTGC TCATTGCCAT GTTCAGTTAC 660  
 ACATTGCGCA AAGTACAGGG CAACAGCGAT CTCTACTGGA AGGCGCAGCG TTACCGCCTC 720  
 ATCCGGGAAT TCCACTCTCG GCCCGCGCTG GCGCGGCCCT TTATCGTCAT CTCCCACTTG 780  
 CGCTCCTGTC TCAGGCAATT GTGCAGGCGA CCGCGGAGCC CCCAGCCGTC CTCCCGGCC 840  
 CTCGAGCATT TCGGGTTTA CTTTCTAAG GAAGCCGAGC GGAAGCTGCT AACGTGGGAA 900  
 TCGGTGCATA AGGAGAACTT TCTGCTGGCA CGCGTAGGG ACAAGCGGGA GAGCGACTCC 960  
 GAGCGTCTGA AGCGCACGTC CCAGAAGGTG GACTTGGCAC TGAAACAGCT GGCACACATC 1020  
 CGCGAGTACG AACAGCGCCT GAAAGTGCTG GAGCGGGAGG TCCAGCAGTG TAGCCGCGTC 1080  
 CTGGGGTGGG TGGCCGAGGC CCTGAGCCGC TCTGCCTTGC TGCCCCAGG TGGGCCGCCA 1140  
 CCCCCTGACC TGCTTGGGTC CAAAGACTGA GCCCTGCTGG CGGACTTCAA GGAGAAGCCC 1200  
 CCACAGGGGA TTTTGCTCCT AGAGTAAGGC TCATCTGGGC CTCGGCCCCC GCACCTGGTG 1260  
 GCCTTGTCCT TGAGGTGAGC CCCATGTCCA TCTGGGCCAC TGTCAGGACC ACCTTTGGGA 1320  
 GTGTATCCT TACAAACCAC AGCATGCCCC GCTCCTCCCA GAACCAGTCC CAGCCTGGGA 1380  
 GGATCAAGGC CTGGATCCCG GGCCGTTATC CATCTGGAGG CTGCAGGGTC CTTGGGGTAA 1440  
 CAGGGACCAC AGACCCCTCA CCACTCACAG ATTCTCACA CTGGGGAAAT AAAGCCATT 1500  
 CAGAGCAAAA AAAAAAAAAA AAAA 1524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3410 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGCAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCCTGGT	480
CTGTGTCCCG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCCGA	TCCCAGGCCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCCTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	AQCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCTT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCAG	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCCTGC	TCACCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTCGCCC	CACTGCTGTC	CATGCCGGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCGG	CTGCACCAGC	TGTGCTGCCG	1080
CATGCCCCGC	ACCCTGCGCC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTACA	CGGATTTTCG	GGGCGAGGGG	CTGTACCAGG	GCGTGCCCAG	1200
AGCTGAGCCG	GGCACCAGAG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGCAGCCT	1260
GGGGCTGTTT	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTG	GGCACTCGAG	CAGTCTATTT	GGCCAGTGTG	GCAGCTTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTACCTTTC	TCAGCCTGTC	AGATCCTGCC	CTACACACTG	GCCTCCCTCT	ACCACCGGGA	1500
GAAGCAGGTG	TTCTTGCCCA	AATACCGAGG	GGACACTGGA	GGTGCTAGCA	GTGAGGACAG	1560
CCTGATGACC	AGCTTCTCTG	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCCACC	TCCACCCGCG	CTCTGCGGGG	CCTCTGCCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGT	CTGGACCTCG	CCATCCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTTT	ATGGGCTCCA	TTGTCCAGCT	CAGCCAGTCT	GTCAGTGCCT	ATATGGTGTC	1860
TGCCGCAGGC	CTGGGTCTGG	TCGCCATTTA	CITTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGGG	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GCCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTTCCCATC	TCTAAGCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	GAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTTG	TAGGGGAAGA	2460

GTCCTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC CACAGCACTG TCTTTTTGCT 2520  
 GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCCTCT GTTGCCATCA 2580  
 CAGAGACACA GGCATTTAAA TATTTAACTT ATTTATTTAA CAAAGTAGAA GGAATCCAT 2640  
 TGCTAGCTTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA 2700  
 GGTCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT CTCCTGGGGT 2760  
 CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC TACTCATCCC AAATGATAAT 2820  
 TCCAAATGCT GTTACCCAAG GTTAGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT 2880  
 CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTGGGCCAG CCTGGTTCCC CCCACTTCCA 2940  
 CTCCCCTCTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCAAAAT TTCCCCTACC 3000  
 CCAACTTTTC CCCTACCCCC AACTTTCCCC ACCAGTCCA CAACCTGTT TGGAGCTACT 3060  
 GCAGGACCAG AAGCACAAG TGCGGTTTCC CAAGCCTTTG TCCATCTCAG CCCCAGAGT 3120  
 ATATCTGTGC TTGGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG 3180  
 GAGGTCTTAT CTCTCAGGGG GGGTTTAAAGT GCCGTTTGCA ATAATGTGCT CTTATTTATT 3240  
 TAGCGGGGTG AATATTTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA 3300  
 AAATTAAAGG CTTTCTTATA TGTTTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAATAA AAAAAAAAAA 3410

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1289 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCCTTT 60  
 GTGGAGCCTC AGCAGTTCCC TCTTTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA 120  
 CCATGCAGTG CTTCAGCTTC ATTAAGAACA TGATGATCCT CTTCAATTGG CTCATCTTTC 180  
 TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCGTTTC 240  
 TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC 300  
 TCATCGCAGC CGGCGTTGTG GTCTTTGCTC TTGGTTTCTT GGGCTGCTAT GGTGCTAAGA 360  
 CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CECTCTCATC TCGATTGCTG 420  
 AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCCTGACGT 480  
 TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGTTTCCCA GGAAGACTTC ACTCAAGTGT 540  
 GGAACACCAC CATGAAAGGG CTCAAGTGCT GTGGCTTCCAC CAACTATACG GATTTTGAGG 600  
 ACTCACCTTA CTCAAAGAG AACAGTGCCT TTCCCCTATT CTGTTGCAAT GACAACGTCA 660  
 CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAA GTAGAGGGTT 720  
 GCTTCAATCA GCTTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG 780  
 CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC 840  
 TACAATAAGT CCACTTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACT GTGAAGAGGC 900  
 ACCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA 960  
 GAATGGACCT GCCCTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTTAGCG 1020  
 ATGCCTGACT TTCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080  
 GTAGCCAGTT CTGTTGCCCA TTCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC 1140  
 TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200  
 AAGTGAAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC 1260  
 TGTTACAATG TTAATAAAAA AAAAAAAAAA 1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1           5           10           15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
          20           25           30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35           40           45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50           55           60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65           70           75           80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
          85           90           95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
          100           105           110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
          115           120           125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
          130           135           140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
          145           150           155           160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
          165           170           175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
          180           185           190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
          195           200           205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

```



210 215 220  
 Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
 225 230 235 240  
 Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
 245 250 255  
 Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
 260 265 270  
 Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
 275 280 285  
 Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290 295 300  
 Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15  
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30  
 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45  
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60  
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80  
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95  
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
 115 120 125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190  
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205  
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
530 535 540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
20 25 30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
35 40 45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
 85 90 95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
 115 120 125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
 130 135 140  
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
 145 150 155 160  
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
 165 170 175  
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
 180 185 190  
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
 195 200 205  
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
 210 215 220  
 Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 225 230 235 240  
 Gln

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTTCTC	TCCCCTCCTC	TGAATTTAAT	TCTTTCAACT	TGCAATTTGC	AAGGATTACA	60
CATTTCACTG	TGATGTATAT	TGTGTTGCAA	AAAAAAAAAA	GTGTCTTTGT	TTAAAATTAC	120
TTGGTTTGTG	AATCCATCTT	GCTTTTFCCT	CATTGGAAC	AGTCATTAAC	CCATCTCTGA	180
ACTGGTAGAA	AAACATCTGA	AGAGCTAGTC	TATCAGCATC	TGACAGGTGA	ATTGGATGGT	240
TCTCAGAACC	ATTTACCCA	GACAGCCTGT	TTCTATCCTG	TTTAATAAAT	TAGTTTGGGT	300
TCTCTACATG	CATAACAAAC	CCTGCTCCAA	TCTGTCACAT	AAAAGTCTGT	GACTTGAAGT	360
TTAGTC						366

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA	ACCATTTCCT	ATATTATAGC	AAAATTAAAA	TCTACCCGTA	TTCTAATATT	60
GAGAAATGAG	ATNAAACACA	ATNTTATAAA	GTCTACTTAG	AGAAGATCAA	GTGACCTCAA	120
AGACTTTACT	ATTTTCATAT	TTTAAGACAC	ATGATTATC	CTATTTAGT	AACCTGGTTC	180
ATACGTTAAA	CAAAGGATAA	TGTGAACAGC	AGAGAGGATT	TGTTGGCAGA	AAATCTATGT	240
TCAATCTNGA	ACTATCTANA	TCACAGACAT	TTCTATTCCT	TT		282

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG	CTTCACTGCC	TTCTTAGATG	CTTCTGGTCA	ACATANAGGA	ACAGGGACCA	60
TATTTATCCT	CCCTCCTGAA	ACAATTGCAA	AATAANACAA	AATATATGAA	ACAATTGCAA	120
AATAAGGCAA	AATATATGAA	ACAACAGGTC	TCGAGATATT	GGAAATCAGT	CAATGAAGGA	180
TACTGATCCC	TGATCACTGT	CCTAATGCAG	GATGTGGGAA	ACAGATGAGG	TCACCTCTGT	240
GACTGCCCCA	GCTTACTGCC	TGTAGAGAGT	TTCTANGCTG	CAGTTCAGAC	AGGGAGAAAT	300
TGGGT						305

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTC CCGCACAATC TGAGTGAAAA 60  
AANTCCTGGG T 71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA 60  
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC 120  
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCAC TAANC GGAATTAANT 180  
AATGGANTCA AGANACTCCC AGGCCCTCAGC GT 212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60  
CTCCGCCGGC GCAGAACATG CTGGGGTGGT 90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTTGA 60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTCTGAAG 120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCCTTTG GGAATTCCTT TACGATNGCC 180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA 218
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG 60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT 120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T 171
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA 60
TTATCAANTA TTGTGT 76
```

(2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT    60
CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG    120
TTAAGATTGG T                                     131
```

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG    60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA    120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT    180
TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG    240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC    300
CATGGTGGGG GTCCTGCATC TGTAAGAATG GAATTGATTT TGCTTTTGCA AGAATCTCAG    360
CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC    420
CTCTTTGCTT GT                                     432
```

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCACCT TTCTAACCAT 60  
 AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTTGT 112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG 54

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTCTAA TGCTCCCGT CTACCAGCTC 60  
 ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGC TCTCTGCTCA 120  
 TTCTCTCTGA AGTCTAGGTT ACCCATTTG GGGACCCATT ATAGGCAATA AACACAGTTC 180  
 CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT 240  
 TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT 300  
 AGGCTGCCTT CTTTCCATG TCC 323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTTCATC	120
TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTFTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTTCCATTG TGTTTGGCCG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTTTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTTATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTGGTTGT AAAGCTCTTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAT CTGATGTGAT TTGGTTTATT ATCCAATAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA TTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC	60
AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT	120
CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT	180
TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG	240
GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT	300
GTAACAATCT ACAATTGGTC CA	322

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC ACAAGTTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT	60
CTTGTTTTTC TTTCCATCTG GCTCCTGGGT TGACAATTG TGGAAACAAC TCTATTGCTA	120
CTATTTAAAA AAAATCACAA ATCTTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCCCTG	180
CTATTCCTGT TTTGTCAAAG AAATTATATT TTTCAAAATA TGTNTATTG TTTGATGGGT	240
CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG	278

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GTTTANAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAAACA      60
TGATTCTCTG AGGTTAAACT TGGTTTTCAA ATGTTATTTT TACTTGATT TTGCTTTTGG      120
T                                          121

```

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

ACTTANAACC ATGCCTAGCA CATCAGAATC CCTCAAAGAA CATCAGTATA ATCCTATACC      60
ATANCAAGTG GTGACTGGTT AAGCGTGCGA CAAAGGTCAG CTGGCACATT ACTTGTGTGC      120
AAACTTGATA CTTTGTGTTCT AAGTAGGAAC TAGTATACAG TNCCTAGGAN TGGTACTCCA      180
GGGTGCCCCC CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACTTTCGCT      240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAC GTTTGCTGAG      300
TTCCCAAGGA TGCAAGCCT GGTGCTCAAC TCCTGGGGCG TCAACTCAGT      350

```

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT      60
GCTGTGATTG TATCCGAATA NTCCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT      120
GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA      180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAACNCCAAG      240
AAAAGTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC      300
TCCAGGAAC CCGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCCCAC TGGCGTGATG      360
GGTGCAGANG GATGAAGCAG CCAGNTGTTC TGCTGTGGT      399

```

## (2) INFORMATION FOR SEQ ID NO:137:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTGGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACTTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCCAA	120
TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGG GGGCTGGGGG CATANANGGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTGGCCAC TGTACATTCC CCATNTTTAA	300
AAAAACTGAT GCCTTTTTTT TTTTTTTTTT TAAAATTC	338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA	120
ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACC GCC TATCATCTGC	180

ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG 240  
 CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT 300  
 GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCTACCA CTGCTGAGTG 360  
 GCCTGGAAGT TGTTTAAAGT GT 382

## (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTTCTGTTG TGTNGATTT TACTATAGGG GTTNGCTTN TTCTAAANAT 60  
 ACTTTTCATT TAACANCTTT TGTAAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG 120  
 TTTTCACATT TCAACTTGTA TGTGTTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTT 180  
 ATATTCAGCA TAAAGGAGAA 200

## (2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAACACAT AGAAAAATAA AGTTTGGTGG 60  
 GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT 120  
 ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA 180  
 AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG 240  
 TTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG 300  
 ATTACAAAC CAAGTAATTT TAAACAAAGA CACTT 335

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGATTTTA	60
GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC AACAACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA	360
AGCTACCAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTCACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGATATAT TGCCATCTTT GTCATTTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTTG	120
AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

ACGTAGACCA TCCAAC TTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA      60
ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT      120
GCAGGACAGC TATCATAAGT CGGCCCAGGC ATCCAGATAC TACCATTTGT ATAAACTTCA      180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG      240
TAGTAAATN TTGCTTAGCT GAAACAGCCA CAAAGACTT ACCGCCGTGG TGATTACCAT      300
CAA                                                                303

```

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC      60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTTGC CAACAGGCCT      120
CCAAGTCAGG GCTGGGATT TTTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT      180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC      240
AGACTTGCCC CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG      300
TAGGGGTGAG CTGTGTGACT CTATGGT                                     327

```

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTTCCTG AGGGATAAAT TTCTGATAAA GTCCTGCTGT	120
ATATTCAAGC ACATATGTGA TATATTATTC AGTTCATGT TTATAGCCTA GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACTT TATCTCATCG AATTTTAAAC CCAAACCTCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTTC TACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAAC ACTCTACCAG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTACAATC ACCCCTTTAA TTACCATGCT ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120
GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA	180
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

104

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60
AGCAAGATGG CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG 180
GTGCATCCGG CTCAGT 196
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG 120
GAGGGAGTTT GT 132
```

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 285 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAACCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTGAG	60
CTTCTGCTCT TATGTCCTCA TCTGACAACT CTTTACCATT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 333 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTAGCTC CCCTCCTCCG TCGAACGAGA CTCTGATTTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 308 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACTGT AAAGTGCCTA ACACATGATC GATGATTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240
GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG	300
GCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAAC TGA	120
GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT	180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTTCA AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

ACCCACTGGT CTTGGAACA CCCATCCTTA ATACGATGAT TTTCTGTCTG TGTGAAAATG 60
AANCCAGCAG GCTGCCCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT 120
GCCTGGGTAA TTCACCATTA ATTTCTCTCC CCAAATCTCT TGAGTCTTCC CTTAATATTT 180
CTGTTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA 240
NATGTTTGTA GCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG 300
CCAACCCTGT TTTCCAGTC CACGTAGACA GATTCAGAGT GCGGAATTCT GGAAGCTGGA 360
NACAGACGGG CTCTTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG 420
TGTTTATTCT CTGATGTCCT GT 442

```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAACTG ATGGGTGACG TTGTAGGTTT 60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG 120
GCTGCTGTGG ACTGTTGTTG ATTCCTCACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG 180
GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC 240
TGCTGTGGTG CCGGGANGTG AANGTGTGTT GTCATTGAG CTTGGCCAGC TCTGGAAAGT 300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTAA 360
CGAACCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCTN 420
TCAGGTAANA ATGTGGTTTC AGTGTCCTTG GGCNGCTGTG GAAGGTTGTA NATTGTCAAC 480
AAGGGAATAA GCTGTGGT 498

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACCTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC 60  
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT 120  
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC 180  
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCCC CATGACCCCA GATGCCTCTC 240  
CCACCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTC TAACATCCTG 300  
GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA 360  
CTTGTAGAAT GAAGCCTGGA 380

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA 60  
CACTGTCCAC TGGCCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT 114

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTTA ATATCCTCAT ATATATCAAA 60  
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT 120  
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAACTAC TCACTGT 177

## (2) INFORMATION FOR SEQ ID NO:163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
CATTATACA GACAGGCGTG AAGACATTEA CGACAAAAC GCGAAATTCT ATCCCGTGAC 60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT 120
CATCAGCGGC ATGATGT 137
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA 60
TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA 120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAACTCGG AGTGGCAGAC TGACAACCTGT 180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG 240
GGTTATGACA AAGACAACCTG CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG 300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT 360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT 420
GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACCTT 469
```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```
ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG 60
ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC 120
TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT 180
TCCTCTGAGA TGAGT 195
```

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCTGGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACG CCAAAGAAT	180
TTTGCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCCTTT TTGGTGAAC TTC	383

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:



(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAGT TTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCATCAT CCCTGAGAAG CCCTTCCAG TAGGGTGGGC	180
AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT AACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTTC CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGCCATGG GCAAAGGCCC CTACCACAAA AACAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGGC CATCAGCTGC	420
TCGAACACTG A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTCAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

## (2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA      60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCCTGG TGCATCCGCA GTGGGTGCTG      120
TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG      180
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA      240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC      300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC      360
GCGGGGAAct CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC      420
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC      480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAGAA GGACTCCTGC      540
AACGGTGACT CTGGGGGGGCC CCTGATCTGC AACGGGTACT TGCAGGGCCT TGTGTCTTTC      600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC      660
ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA      720
ATTGACCCCC AAATACATCC TCGGAAGGA ATTCAGGAAT ATCTGTTCCC AGCCCCCTCT      780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC      840
CCCAGCCCCT CTTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCTCC TCCCTCAGAC      900
CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCGCTCCTCC      960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC     1020
CCAACCCNTC ATTCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA     1080
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTTGGC ACGTTGACCC     1140
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTTCCCC TAGATCCAGA AATAAAGTTT     1200
AAGAGAAGNG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA     1248

```

## (2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1           5           10           15

```

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
20 25 30

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
35 40 45

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
50 55 60

Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu  
65 70 75 80

Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe  
85 90 95

Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser  
100 105 110

Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe  
115 120 125

Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn  
130 135 140

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:173: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAAGCC	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCTTGCTT	CGCTAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCCTAC	CGCGGGGAAC	TCTTGCTCTG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTGTCTG	CCCTCTTCAA	GGAGGTCCTC	TGCCCAGTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCCAG	GCAGAATGCC	TACCGTGCTG	CAGTGCCTGA	480
ACGTGTCTGG	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCEGCTG	TACCACCCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCCGTAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCAGTGAG	TGGATAGAGA	720

AAACCGTCCA	GGCCAGTTAA	CTCTGGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGCGGA	AGGAATTCAG	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGCCCC	CAGCCCCTCC	TCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCTCCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCTC	CTCCCTCAGA	CCCAGGGGTT	1020
GAGGCCCCCA	ACCCCTCCTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAGGTC	CCAGCCCCTC	TTCCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTTTCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTTTCATTTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAA						1265

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAGTGAG	TGCAGAGCTC	CTACACCATC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCTTGC	TGGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGCGGGGAA	CTCTTGCCCT	GTTTCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGTCT	GCCCTCTTCA	AGGAGGTCCCT	CTGCCCAGTC	GCGGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAATGC	CTACCGTGCT	GCAGTGCGTG	AACGTGTCGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAAGCTCT	ATGACCCGCT	GTACCACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGCGACT	540
CAGGGAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGGCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATTT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTGTGTTGA	ATTTTTTGAT	ATTTCTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATTG	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGCAG	GGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAAGCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGTTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGGC	AACAGAGTAA	GACTCTGTCT	1440
CAAAAAAAA	AAAAAAAAA					1459

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTCGCTC GGGCGTCTTG      60
GTGCATCCGC AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCCTGC ACAGTCTTGA GGCCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCTTGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAACTC TTGCCTCGTN TCTGGCTGGG GTCTGCTGGE GAACGGCAGA      360
ATGCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCAGCATG TTCTGCGCCG GCGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGGGGGGCCC CTGATCTGCA ACGGGTACTT GCAGGGCCTT      540
GTGTCTTTTC GAAAAGCCCC GTGTGGCCAA CTTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTCa CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCTCCTC CCTCAGGCC AGGAGTCCAG GCGCCAGCC CCTCCTCCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCTC CTCCCTCAGA CCCAGGAGTC CAGACCCCCC AGCCCTCCT      840
CCNTCAGACC CAGGAGTCCA GCCCCTCCTC CNTCAGACGC AGGAGTCCAG ACCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGGTGCAGGC CCGCAACCCG TCNTCCNTCA GAGTCCAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC      1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TTTCCCTGTA CACAGTCCCC CTTGTGGCA      1080
NGTTGACCCA ACCTTACCAG TTGGTTTTTC ATTTTTTGTC CCTTCCCCT AGATCCAGAA      1140
ATAAAGTNTA AGAGAAGCGC AAAAAAA

```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp

1

5

10

15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu

20

25

30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val

35                      40                      45  
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu  
 50                      55                      60  
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65                      70                      75                      80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85                      90                      95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100                      105                      110  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115                      120                      125  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130                      135                      140  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145                      150                      155                      160  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165                      170                      175  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180                      185                      190  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195                      200                      205

## (2) INFORMATION FOR SEQ ID NO:177:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1119 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC AGCCCTGGCA GCGGGCACTG GTCATGGAAA ACGAATTGTT CTGCTCGGGC	60
GTCCTGGTGC ATCCGCAGTG GGTGCTGTCA GCCGCAGACT GTTCCAGAA CTCCTACACC	120
ATCGGGCTGG GCCTGCACAG TCTTGAGGCC GACCAAGAGC CAGGGAGCCA GATGGTGGAG	180
GCCAGCCTCT CCGTACGGCA CCCAGAGTAC AACAGACCCT TGCTCGCTAA CGACCTCATG	240
CTCATCAAGT TGGACGAATC CGTGTCCGAG TCTGACACCA TCCGGAGCAT CAGCATTGCT	300
TCGCAGTGCC CTACCGCGGG CAACTCTTGC CTCGTTTCTG GCTGGGGTCT GCTGGCGAAC	360
GATGCTGTGA TTGCCATCCA GTCCCAGACT GTGGGAGGCT GGGAGTGTGA GAAGCTTTCC	420
CAACCCTGGC AGGGTGTAC CATTTCGGCA ACTTCCAGTG CAAGGACGTC CTGCTGCATC	480

```

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG      540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGTCTATTGT      600
ACTAACCATG CCGATGTTTA GGTGAAATTA GCGTCACTTG GCCTCAACCA TCTTGGTATC      660
CAGTTATCCT CACTGAATTG AGATTTCCTG CTTCAGTGTG AGCCATTCCC ACATAATTTC      720
TGACCTACAG AGGTGAGGGA TCATATAGCT CTTCAGGAT GCTGGTACTC CCCTCACAAA      780
TTCATTTCTC CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCCAGGG TGGGTGTGCA      840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTTAA ATCCCTCATG      900
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTTAGT GTATGCTGTC CATTATGCA      960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCTTGGG    1020
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC    1080
TTAATAAACA GAAGCTGTGA TGTAAAAAAA AAAAAAAAAA    1119

```

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1           5           10           15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100         105         110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115         120         125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130         135         140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser

```

145

150

155

160

Pro Gly Thr Leu

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60  
 CCAGCTGCCC CCGGCCCGGG GATGCGAGGC TCGGAGCACC CTGCCCCGGC TGTGATTGCT 120  
 GCCAGGCACT GTTCATCTCA GCTTTTCTGT CCCTTTGCTC CCGGCAAGCG CTTCTGCTGA 180  
 AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA 240  
 AAAAAAAAAA 250

## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA 60  
 TCACCCAGAC CCGGCCCTG CCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA 120  
 CTCTGCTACT CGGAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTT TATAAATGCC 180  
 TGATTTAAAA AAAAAAAAAA 202

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG 60  
 AATGTTTAGG CAGTGCTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT 120  
 TTATTCCTCT TTCTTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA 180  
 GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA 240  
 AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTGAAC 300  
 CTACTCTGTT CCTTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTTT GGAAGCCAA 360  
 ATTGATAATA TTCTATGTTT TAAAAGTTGG GTATACATA AATTATTAAG AAATATGGAW 420



TTTTATTCCC AGGAATATGG KGTTTCATTTT ATGAATATTA CSCRGGATAG AWGTWTGAGT 480  
 AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTT 540  
 CAAAAAAAAA AAAAAAAAAA 558

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTTTGA TCCAACCCTG GCTTWTTTTC 60  
 AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG 120  
 CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG 180  
 TTWCAATTC ACGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA 240  
 CTAAGGTAA ACTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA 300  
 TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT 360  
 NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGG TACGCATARA 420  
 AWTGSTGARA AAATTAATAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAAAA 479

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC 60  
 AGTACCAGTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCAGTGCT 120  
 GGTGCCAGCC TGACCGCCAC TCTCACATTT GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT 180  
 GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTCCTCCT ACAAGTGAGA TTTTAGATAT 240  
 TGTTAATCCT GCCAGTCTTT CTCTTCAAGC CAGGGTGCAT CCTCAGAAAC CTACTCAACA 300  
 CAGCACTCTA GGCAGCCACT ATCAATCAAT TGAAGTGGAG AGTCTGCATT ARATCTATTT 360  
 GCCATTTCAA AAAAAAAAAA AAAA 384

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYNT CCRGTATKAC CTCAACGAGC 60

```

AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG 120
CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA 180
AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC 240
TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTCGGACTG 300
TGAGCCCTGA TGCCTTTTTG CCAGCCATAC TCTTTGGCAT CCAGTCTCTC GTGGCGATTG 360
ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCATA AAGGGAACAC ATTTGACTTT 420
TTTTCTCAT ATTTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAACTST 480
TAAAAAATAA AAAAAA 496

```

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC 60
CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC 120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTCGGAG CCCGGCTTCT 180
GGGCACACCC TCCTGGGGCC CAGGCGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG 240
TGGTGCTGCT CCTCGTCATC TTCCTGCTCG TGGCCAACAT CCTGCTGGTC AACTTGCTCA 300
TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG 360
CGCGAGCGTT ACCGCCTCAT CCGG 384

```

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC 60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT 120
CCAGGAAACT CTCAATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTTCCGC 180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT 240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAG CTCTCTGACA GTGAGGTCAC 300
CAGCCCTATC ATGCCGTTGA MCGTGCCGAA GARCACCGAG CCTTGTGTGG GGGKKGAAAGT 360
CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGGCAAAAG ACATTGACAA ACTCGCCAG 420
GTGGAAAAAG AMCAMCTCCT GGARGTGCTN GCCGCTCCTC GTCMGTGGT GGCAGCGCTW 480
TCCTTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC 540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT 577

```

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTPCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGSTG AGAATYCATW	60
ACTKGGAAAA GMAACATTAA AGCCTGGACA CTGGTATTAA AATTCACAAT ATGCAACACT	120
TTAAACAGTG TGTCAATCTG CTCCCYYNAC TTTGTCTATCA CCAGTCTGGG AAKAAGGGTA	180
TGCCCTATTC ACACCTGTTA AAAGGGCGCT AAGCATTTTT GATTCAACAT CTTTTTTTTT	240
GACACAAGTC CGAAAAAGC AAAAGTAAAC AGTTATYAAT TTGTTAGCCA ATTCACCTTC	300
TTTCATGGGAC AGAGCCATYT GATTTAAAAA GCAATTGCA TAATATTGAG CTTYGGGAGC	360
TGATATTTGA GCGGAAGAGT AGCCTTTCTA CTTCACCAGA CACAACCTCC TTCATATTG	420
GGATGTTNAC NAAAGTWATG TCTCTWACAG ATGGGATGCT TTTGTGGCAA TTCTGTTCTG	480
AGGATCTCCC AGTTTATTTA CCACTTGCAC AAGAAGGCGT TTTCTTCTC TAGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATCTTTTT TACTTTTGTA AAAGCTTATG	120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTCGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTKGACKARG	300
GGGGACAAAG AAAAGCAAAA CTGAMCATAA RAAACAATWA CCTGGTGAGA ARTTGCAATA	360
ACAGAAATWR GGTAGTATAT TGAARNACAG CATCATTAAA RMGTTWKTF WTTCTCCCTT	420
GCAAAAAACA TGTACNGACT TCCCGTTGAG TAATGCCAAG TTGTTTTTT TATNATAAAA	480
CTTGCCCTTC ATTACATGTT TNAAGTGGT GTGGTGGGCC AAAATATTGA AATGATGGAA	540
CTGACTGATA AAGCTGTACA AATAAGCAGT GTGCCTAACA AGCAACACAG TAATGTTGAC	600
ATGCTTAATT CACAAATGCT AATTTCAATTA TAAATGTTTG CTAAAATACA CTTTGAACATA	660
TTTTTCTGTN TTCCAGAGC TGAGATNTTA GATTTTATGT AGTATNAAGT GAAAAANTAC	720
GAAAATAATA ACATTGAAGA AAAANANAAA AAANAAAAAA A	761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT TTTGCCGATN CTAATTTTT ATTGCAGGAN GTGGGGGTGT ATGCACCGCA	60
CACCGGGGCT ATNAGAAGCA AGAAGGAAGG AGGGAGGGCA CAGCCCCTTG CTGAGCAACA	120
AAGCCGCTG CTGCCTTCTC TGTCTGTCTC CTGGTGCAGG CACATGGGGA GACCTTCCCC	180

```

AAGGCAGGGG CCACCAGTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG 240
TGATAGGCAC AGGCCACCCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTCGACCAG 300
GTCAATTGTGC CBTGCCCAGG CACAGCGTAN ATCTGGAAAA GACAGAATGC TTTCCTTTTC 360
AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTTNG GCTNGGTCTT GGTACNCTTG 420
GTTCGGCCCA GCTECNCGTC CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCNGGNCCC 480
CC 482

```

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

TTTTTTTTTT TTTTAAACA GTTTTTCACA ACAAATTTA TTAGAAGAAT AGTGGTTTGT 60
AAAACCTCTCG CATCCAGTGA GAACCTACCAT ACACCACATT ACAGCTNGGA ATGTNCTCCA 120
AATGTCTGGT CAAATGATAC AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAAG 180
CGCTTTTGAC ATACAATGCA CAAAAAAAAA AGGGGGGGGG GACCACATGG ATTAATAATT 240
TAAGTACTCA TCACATACAT TAAGACACAG TTCTAGTCCA GTCNAAAATC AGAACTGCNT 300
TGAAAAATTT CATGTATGCA ATCCAACCAA AGAACTTNAAT TGGTGATCAT GANTNCTCTA 360
CTACATCNAC CTTGATCATT GCCAGGAACN AAAAGTTNAA ANCACNCNGT ACAAANAANA 420
TCTGTAATTN ANTTCAACCT CCGTACNGAA AAATNTTNTT TATACACTCC C 471

```

## (2) INFORMATION FOR SEQ ID NO:191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

GAGGGATTGA AGGTCTGTTT TASTGTCGGM CTGTTTACGCC ACCAACTCTA ACAAGTTGCT 60
GTCTTCCACT CACTGTCTGT AAGCTTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA 120
ATTCTTCACC AGTCACATCT TCTAGGACCT TTTTGGATTG AGTTAGTATA AGCTCTTCCA 180
CTTCCTTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTACAAAAG AATTYAATTG 240
CTCGTTCTCT AACAATGTCC TCTCCTTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC 300
CTTTGTGCAT CCATTTTAAA TATACTTAAT AGGGCATTGK TNCAC TAGGT TAAATTCTGC 360
AAGAGTCATC TGTCTGCAAA AGTTGCGTTA GTATATCTGC CA 402

```

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATCCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTTGTGGA	AAAAGTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCAAT	GCTTTTGTGC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTTGTTC	CAAAAGCARG	TCTTGGTGCC	420
TGTTGGATCA	GGTTCCCAT	TCCAGTCYG	AATGTTTACA	TGGCATATTT	WACTTCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTTGACT	GAGAACCCTGA	TGCGGTGACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACTCCAY	TCGTGGCTTG	GGGTGACGG	180
TKAAGTGCA	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAG	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCCGAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCCAAGT	TGTCGCGCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGTT	TTTGTCGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCGT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT						608

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCCTC	GCATTGTGCT	TGCTGSCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAAC	240
AACAACAACA	AAATAACATG	TTTGCTGTGT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTT	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

CCSTTKGAGG GGTKAGGKYC CAGTTYCCGA GTGGAAGAAA CAGGCCAGGA GAAGTGCGTG      60
CCGAGCTGAG GCAGATGTTC CCACAGTGAC CCCCAGAGCC STGGGSTATATA GTYTCTGACC      120
CCTCNCAAGG AAAGACCACS TTCTGGGGAC ATGGGCTGGA GGGCAGGACC TAGAGGCACC      180
AAGGGAAGGC CCCATTCCGG GGSTGTTCCC CGAGGAGGAA GGAAGGGGGC TCTGTGTGCC      240
CCCCASGAGG AAGAGGCCCT GAGTCCTGGG ATCAGACACC CCTTCACGTG TATCCCACACA      300
CAAATGCAAG CTCACCAAGG TCCCCTCTCA GTCCCCTTCC STACACCCTG AMCGGCCACT      360
GSCSCACACC CACCCAGAGC ACGCCACCCG CCATGGGGAR TGTGCTCAAG GARTCGCNGG      420
GCARCGTGGA CATCTNGTCC CAGAAGGGGG CAGAATCTCC AATAGANGGA CTGARCMSTT      480
GCTNANAAAA AAAAAANAAA AA                                     502

```

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 665 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC      60
CCTCTGGAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT      120
WAGCTGTTTT GAGTTGATTS GCACCACTGC ACCCACAAC TCAATATGAA AACYAWTTGA      180
ACTWATTTAT TATCTTGTGA AAAGTATAAC AATGAAAATT TTGTTCATAC TGTATTKATC      240
AAGTATGATG AAAAGCAAWA GATATATATT CTTTTATTAT GTTAAATTAT GATTGCCATT      300
ATTAATCGGC AAAATGTGGA GTGTATGTTT TTTTCACAGT AATATATGCC TTTTGTAAC T      360
TCACTTGTTT ATTTTATTGT AAATGARTTA CAAAATTCCT AATTTAAGAR AATGGTATGT      420
WATATTTATT TCATTAATTT CTTTCCTKGT TTACGTWAAT TTTGAAAAGA WTGCATGATT      480
TCTTGACAGA AATCGATCTT GATGCTGTGG AAGTAGTTTG ACCCACATCC CTATGAGTTT      540
TTCTTAGAAT GTATAAAGGT TGTAGCCCAT CNAAC TTCAA AGAAAAAAT GACCACATAC      600
TTTGCAATCA GGCTGAAATG TGGCATGCTN TTCTAATTCC AACTTTATAA ACTAGCAAAN      660
AAGTG                                     665

```

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTTT	TTTTTTTTTGC	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTTCAA	AAGATTAAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACCTTTAG	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGATTTTT	GTTCACTNCTG	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTTCANTCT	GTANNAANTA	TTTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGNTTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAAAAT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTGAG	TTCCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTTNGG	CTGGGGACCA	TCCCATTGAA	CGTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCNNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCAGACGAA GATTCTGCCA GCAGTTGGTC      60
CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC      120
AAGGCTGAGC TGACGCGGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA      180
CAGCCGGAAC AGAGCCCGGT GAANGCGGGA GGCCTCGGGG AGCCCCTCGG GAAJGGCGGC      240
CCGAGAGATA CGCAGGTGCA GGTGGCCGCC

```

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA      60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCLG GTCAACTTCC TTIGTCGTGG      120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAANCGAAGC ANAANTAACA      180
TGGAGTGGGT GCACCCTCCC TGTAGAACCT GGTTACNAAA GCTTGGGGCA GTTCACCTGG      240
TCTGTGACCG TCATTTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG      300
TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAAA ATCCACNTGA      360
AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA      419

```

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

TTTNTTTTTT TTTTNTTTTT TTTTNTTTTT TTTTNTTTTT TTTTNTTTTT TTTTNTTTTT      60
TGGCACTTAA TCCATTTTTA TTTCAAAATG TCTACAAANT TTNAATNCNC CATTATACNG      120
GTNATTTTNC AAAATCTAAA NNTTATTCAA ATNTNAGCCA AANTCCTTAC NCAAAATNNA      180
TACNCNCAAA AATCAAAAAT ATACNTNTCT TTCAGCAAAC TTNGTTACAT AAATTAAAAA      240
AATATATACG GCTGGTGTTF TCAAAGTACA ATTATCTTAA CACTGCAAAC ATNTTTNNA      300
GGAACATAAA TAAAAAATAA CACTNCCGCA AAGGTATAAG GGAACAACAA ATTCTNTTTA      360
CAACANCNNC NATTATAAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTACACNG      420
GGATCTTAAC TTTTACTNCA CTTTGTATTAT TTTTNTANAA CCATTGTNTT GGGCCCAACA      480
CAATGGNAAT NCCNCCNCNC TGGACTAGT

```



## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

TTTTTTTTTT TTTTTTTTGA CCCCCCTCTT ATAAAAAACA AGTTACCATT TTATTTTACT 60
TACACATATT TATTTTATAA TTGGTATTAG ATATTCAAAA GGCAGCTTTT AAAATCAAAC 120
TAAATGGAAA CTGCCTTAGA TACATAATTC TTAGGAATTA GCTTAAAATC TGCCTAAAGT 180
GAAAATCTTC TCTAGCTCTT TTGACTGTAA ATTTTGTACT CTTGTAAAAC ATCCAAATTC 240
ATTTTCTTG TCTTAAAAT TATCTAATCT TTCCATTTTT TCCCTATTCC AAGTCAATTT 300
GCTTCTCTAG CCTCATTTCC TAGCTCTTAT CTACTATTAG TAAGTGGCTT TTTTCCTAAA 360
AGGGAAAACA GGAAGAGANA ATGGCACACA AAACAAACAT TTTATATTCA TATTTCTACC 420
TACGTTAATA AAATAGCATT TTGTGAAGCC AGCTCAAAAG AAGGCTTAGA TCCTTTTATG 480
TCCATTTTAG TCACTAAACG ATATCNAAG TGCCAGAATG CAAAAGGTTT GTGAACATTT 540
ATTCAAAGC TAATATAAGA TATTCACAT ACTCATCTTT CTG 583

```

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

TTTTTTTTINT TTTTTTTTTT TTTTTTNTCT TTCTTTTTTT TTGANAATGA GGATCGAGTT 60
TTTCACTCTC TAGATAGGGC ATGAAGAAAA CTCATCTTTC CAGCTTTAAA ATAACAATCA 120
AATCTCTTAT GCTATATCAT ATTTTAAGTT AACTAATGA GTCCTGGCT TATCTTCTCC 180
TGAAGGAAAT CTGTTCAATC TTCTCATTCA TATAGTTATA TCAAGTACTA CCTTGCATAT 240
TGAGAGGTTT TTCTTCTCTA TTTACACATA TATTTCCATG TGAATTTGTA TCAAACCTTT 300
ATTTTCATGC AACTAGAAA ATAATGINTT CTTTTCGATA AGAGAAGAGA ACAATATNAG 360
CATTACAAAA CTGCTCAAAT TGTTTGTTAA GNTTATCCAT TATAATTAGT TNGGCAGGAG 420
CTAATACAAA TCACATTTAC NGACNAGCAA TAATAAACT GAAGTACCAG TTAAATATCC 480
AAAATAATTA AAGGAACATT TTTAGCCTGG GTATAATTAG CTAATTCAT TTACAAGCAT 540
TTATTNAGAA TGAATTCACA TGTATTATT CCNTAGCCCA ACACAATGG 589

```

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTNTTTTT	TTTTTTCAGT	AATAATCAGA	ACAATATTTA	TTTTTATATT	TAAAATTCAT	60
AGAAAAGTGC	CTTACATTTA	ATAAAAGTTT	GTTTCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTGAAAAGA	TAAAATTTGA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAAA	TAAATTACTA	TGGACTTCTT	GCTTTAATTT	TGTGATGAAT	300
ATGGGGTGTC	ACTGGTAAAC	CAACACATTC	TGAAGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAGT	TTCTCTTTCT	TCAATCTTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTTT	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TGCCAATAT	TAAAAAATA	ATAATGTTTA	CTACTAGTGA	540
AACCC						545

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTTAGTC	AAGTTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATTT	60
CATTTATTAG	CTCTGCAACT	TACATATTTA	AATTAAAGAA	ACGTTNTTAG	ACAACTGTNA	120
CAATTTATAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAATTC	TCTTCTCCAT	CCCCATGNG	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAAG	ATGAAGCTAG	GCNTGGGCTT	360
TCGGTGAAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCCTTCCT	CAAAGGCNGC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTTANAA	CTAGCAACTC	TTATTTCTTT	CCTTTAAAAA	60
TACATAGCAT	TAAATCCCAA	ATCCTATTTA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCAATTTATAG	GACCTTCTGG	TGGTCTGTCT	GTTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTTGCAT	GCAGAGGAGG	TAAAAGGTAT	TGGATTTTCA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAAGAAGGC	AGCCTAGGCC	CTGGGGAGCC	CA			332

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

AGGGCGTGGT GCGGAGGGCG TTACTGTTTT GTCTCAGTAA CAATAAATAC AAAAAGACTG      60
GTTGTGTTCC GGGCCCATCC AACCACGAAG TTGATTTC TC TTGTGTGCAG AGTGACTGAT      120
TTTAAAGGAC ATGGAGCTTG TCACAATGTC ACAATGTCAC AGTGTGAAGG GCACACTCAC      180
TCCCGCGTGA TTCACATTTA GCAACCAACA ATAGCTCATG AGTCCATACT TGTAAATACT      240
TTTGGCAGAA TACTTNTTGA AACTTGCAGA TGATAACTAA GATCCAAGAT ATTTCCCAAA      300
GTAAATAGAA GTGGGTCATA ATATTAATTA CCTGTTTACA TCAGCTTCCA TTTACAAGTC      360
ATGAGCCCAG ACACTGACAT CAAACTAAGC CCACTTAGAC TCCTCACCAC CAGTCTGTCC      420
TGTCATCAGA CAGGAGGCTG TCACCTTGAC CAAATTCTCA CCAGTCAATC ATCTATCCAA      480
AAACCATTAC CTGATCCACT TCCGTAATG CACCACCTTG GTGA                          524
  
```

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTG TTGCTCCTTG      60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA      120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA                          159
  
```

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC      60
ACTGAATTTT TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA      120
TGGGGAGATT TTANCCAATT TANGINTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT      180
TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA      240
CCAGGATGCT AAATCA                          256
  
```

(2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG    60
ACTGGAACAC ATACCCACAT CTTTGTCTCG AGGGATAATT TTCTGATAAA GTCTTGCTGT    120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA    180
GGGGAGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA    240
AAAAAAGGAG CAAATGAGAA GCCTATATAT TATATATAT TATATATAT TATATATAT    264

```

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA    60
GGATTTAATG TTGTCTCAGC TTGGGCACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG    120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG    180
TTNAATTTCA TTCCCATGGA CTGGGGATCC TTATCATCAG CCAGAGAGAT TGAAATTTA    240
CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA    300
TTTTTTTTTC CTTTATTCCT TTGTCAGA TTTTATTTTC TTTTATTTTC TTTTATTTTC    328

```

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAAGTGAATT CTCTCCAGTT    60
TAAAGCATTG CTCAGTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT    120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT    180
TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT    240
TCTCATCGGT                                     250

```

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

ACCCAGAATC CAATGCTGAA TATTTGGCTT CATTATTCCT AGATTCTTTG ATTGTCAAAG 60
GATTTAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG 120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACCT GCCCGCCAGT 180
TGAATTTTCAT TCCCATGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTTAC 240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT 300
TTTTTTTTTC TTTATTCCTT TGTCAGAGAT GCGATTCATC CATATGCTAN AAACCAACAG 360
AGTGACTTTT ACAAATTC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT 420
ACTTTGCTCT CCCTAATATA CTC 444

```

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAAGTGAATT CTCTCCAGTT 60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT 120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT 180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT 240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA 300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT 360
GGTGCC 366

```

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

CTGTATAAAC AGAACTCCAC TGCANGAGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC 60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTTNC ATTTTTTTAT 120
TAATAAAAAG TNNAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA 180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT 240

```

AATTCTTCCT TCCCTCCTTT

260

## (2) INFORMATION FOR SEQ ID NO:217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG	GTAAGTTTAN	AAATGTTATA	ATTTACAGGAA	NAGGAACGCA	TATAATTGTA	60
TCTTGCCTAT	AATTTTCTAT	TTTAATAAGG	AAATAGCAAA	TTGGGGTGGG	GGGAATGTAG	120
GGCATTCTAC	AGTTTGAGCA	AAATGCAATT	AAATGTGGAA	GGACAGCACT	GAAAAATTTT	180
ATGAATAATC	TGTATGATTA	TATGTCTCTA	GAGTAGATTT	ATAATTAGCC	ACTTACCCCTA	240
ATATCCTTCA	TGCTTGTAAG	GT				262

## (2) INFORMATION FOR SEQ ID NO:218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG	TGCATTACCG	GAANTGGATC	AANGACACCA	TCGTGGCCAA	CCCCTGAGCA	60
CCCCTATCAA	CTCCCTTTTG	TAGTAAACTT	GGAACCTTGG	AAATGACCAG	GCCAAGACTC	120
AGGCCTCCCC	AGTTCTACTG	ACCTTTGTCC	TTANGTNTNA	NGTCCAGGGT	TGCTAGGAAA	180
ANAAATCAGC	AGACACAGGT	GTAAA				205

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG	TCTCAGTAAC	AATAAATACA	AAAAGACTGG	TTGTGTTCCG	GCCCCATCCA	60
ACCACGAAGT	TGATTTCTCT	TGTGTGCAGA	GTGACTGATT	TTAAAGGACA	TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTTAC ATTTCTTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTGTC GATATTCCT TCATCTTGA TTCCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCACTAC CTTCCCTGAC GTCCTCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCTCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTGG CATAATCCAA	180
TTTCTCTTT TATATTTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCITTTACA TATATCTGGC ATATTGAGT	300
CTCGTATCAA AACAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	351

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAGAAAA ATTATCTTAG GGA	60
CTGATAT TGGTAATTAT GGTCAATTTA ATWRTTTKT GGGGCATTTC CTTACATTGT	120
CTTGACAAGA TTAAAATGTC TGTGCCAAAA TTTTGTATTT TATTTGGAGA CTTCTTATCA	180
AAAGTAATGC TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG	240
TGTGCTATTC TAAAAGATTT TGATTTCTCTG GAATGACAAT TATATTTTAA CTTTGGTGGG	300
GGAAANAGTT ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTG	360
CTTGTTTTG ACCATTAAAGC TATATGTTTA AAA	383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCATCA AAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320



## CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:
  - (a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
  - (b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.
2. The method of claim 1, wherein the binding agent is a monoclonal antibody.
3. The method of claim 2 wherein the binding agent is a polyclonal antibody.
4. A method for monitoring the progression of prostate cancer in a patient, comprising:
  - (a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;
  - (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;
  - (c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.
10. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies of claim 5; and
  - (b) a detection reagent.
11. A diagnostic kit comprising:
- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and
  - (b) a detection reagent.
12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.
13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.
14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.
15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.
16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences, variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

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